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Thanks,
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:36:31 ; Search time 36 Seconds
(without alignments)
2415.330 Million cell updates/sec

Title: US-09-924-338-2

Perfect score: 2275

Sequence: 1 MSSCSGLSRVLVAVATLV.....KPGFLASVLPVDRPGAPNL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2275	100.0	422	Q16542	Q16542 homo sapien
2	1897	83.4	432	Q64385	Q64385 mus musculus
3	1871	82.2	432	P70225	P70225 mus musculus
4	1860.5	81.8	431	Q99MF4	Q99MF4 rattus norv
5	391	17.2	372	O88507	O88507 mus musculus
6	269	11.8	228	O35228	O35228 mus musculus
7	259.5	11.4	229	O75269	O75269 homo sapien
8	255.5	11.2	229	Q14213	Q14213 homo sapien
9	215.5	9.5	881	O57519	O57519 xenopus lae
10	211.5	9.3	422	O75462	O75462 homo sapien
11	210.5	9.3	422	Q9UHH5	Q9UHH5 homo sapien
12	209.5	9.2	425	Q9JMS8	Q9JMS8 mus musculus
13	192	8.4	227	Q9GLW3	Q9GLW3 ursus marit
14	191	8.4	327	O9ET05	O9ET05 marmota mon
15	190.5	8.4	206	Q16354	Q16354 homo sapien
16	190.5	8.4	268	Q8TD78	Q8TD78 homo sapien

17	189.5	8.3	611	13	Q9PTH9	Q9pth9 xenopus lae
18	189	8.3	288	4	Q96P36	Q96p36 homo sapien
19	189	8.3	349	4	Q9UJ35	Q9uhj5 homo sapien
20	189	8.3	376	4	Q96P35	Q96p35 homo sapien
21	187.5	8.2	327	11	Q91ZK7	Q91zk7 sigmodon hi
22	187.5	8.2	625	6	Q9XS92	Q9xs92 trichosurus
23	187.5	8.2	626	13	Q90WG7	Q90wg7 cynops pyrr
24	185.5	8.2	611	13	Q9IBF6	Q9ibf6 xenopus lae
25	185.5	8.2	611	13	Q9PTI0	Q9pti0 xenopus lae
26	185	8.1	346	13	Q93404	Q93404 oreochromis
27	183	8.0	622	6	Q9N0J7	Q9n0j7 callithrix
28	181.5	8.0	636	13	Q90Z16	Q90zi6 paralichthy
29	179.5	7.9	538	13	Q9DFU0	Q9dfu0 sparus aura
30	174.5	7.7	1280	13	Q90933	Q90933 gallus gall
31	174	7.6	608	11	Q99J21	Q99jz1 mus musculus
32	172	7.6	638	13	Q9DE08	Q9de08 oncorhynch
33	161.5	7.1	918	13	Q9W6U9	Q9w6u9 gallus gall
34	159.5	7.0	173	13	Q8QFL5	Q8qfl5 brachydanio
35	156.5	6.9	198	6	O18985	O18985 cervus elap
36	155.5	6.8	1419	13	Q98SW3	Q98sw3 brachydanio
37	153.5	6.7	600	13	Q9PTP0	Q9ptp0 carassius a
38	152.5	6.7	217	6	O46386	O46386 mustela vis
39	152	6.7	604	13	Q8QG54	Q8qg54 cyprinus ca
40	150	6.6	1032	13	Q8UVD6	Q8uud6 brachydanio
41	149.5	6.6	332	11	Q924V5	Q924v5 cavia porce
42	148.5	6.5	1389	13	Q90Z69	Q90z69 brachydanio
43	147	6.5	1256	11	Q925S5	Q925s5 mus musculus
44	146.5	6.4	861	6	Q9BEG2	Q9beg2 bos taurus
45	146	6.4	335	11	Q9QUW1	Q9quw1 mus musculus

ALIGNMENTS

RESULT 1

Q16542 PRELIMINARY; PRT: 422 AA.
AC Q16542: Q14626;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Interleukin-11 receptor (Interleukin 11 receptor, alpha).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MUSCLE;
RX MEDLINE=95399754; PubMed=7670098;
RA Cherel M., Sorel M., Lebeau B., Dubois S., Moreau J.F., Bataille R.,
RA Minvielle S., Jacques Y.;
RT "Molecular cloning of two isoforms of a receptor for the human
RT hematopoietic cytokine interleukin-11.";
RL Blood 86:2534-2540(1995).
RN [2]
RP SEQUENCE FROM N.A.
RA Van Leuven F., Stas L., Hilliker C., Miyake Y., Gossler A.;
RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 3-390 FROM N.A.
RC TISSUE=PLACENTA;
RA Cherel M., Sorel M., Dubois S., Lebeau B., Moreau J., Jacques Y.,
RA Minvielle S.;
RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; U32324; AAB36492.1; -;
DR EMBL; U38102; CAA86224.1; -;
DR EMBL; U32323; AAB36491.1; -;

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DR EMBL; Z46595; CAA86570.1; -.
DR EMBL; BC003110; AA031110.1; -.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003599; Ig_MHC.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; fn3; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 422 AA; 45222 MW; 1F8BC05C139FC326 CRC64;

Query Match 100.0%; Score 2275; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 9e-167;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSCSGLSRVLAVALVATVSVASSPCQAWGPPGVQYQGPGRSVKLCPCPGVTAGDPVSWF 60
DB 1 MSSSCSGLSRVLAVALVATVSVASSPCQAWGPPGVQYQGPGRSVKLCPCPGVTAGDPVSWF 60

QY 61 RDGPKLLQGDPSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVYVSC 120
DB 61 RDGPKLLQGDPSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVYVSC 120

QY 121 QAADYENFSCWSPQSGLTRVLTYSRKTKVILGADSORSPSTGMPWPCQDPPLGAARC 180
DB 121 QAADYENFSCWSPQSGLTRVLTYSRKTKVILGADSORSPSTGMPWPCQDPPLGAARC 180

QY 181 VVHGAEFWSQYRINVTEVNPGLGASTRLDVSLSQILRPDPQGLRVESVPGYPRRLRASW 240
DB 181 VVHGAEFWSQYRINVTEVNPGLGASTRLDVSLSQILRPDPQGLRVESVPGYPRRLRASW 240

QY 241 TYPASWPCQPHFLKFLRYRPAQHPAWSTVEPAGLEEVITDVAAGLPHAVRVVSARDFLD 300
DB 241 TYPASWPCQPHFLKFLRYRPAQHPAWSTVEPAGLEEVITDVAAGLPHAVRVVSARDFLD 300

QY 301 AGTWSTWSPWAMGTPSTGTIPKEIPAWGOLHTQPEVQVDSPPAPPRPSLQPHRLLDHR 360
DB 301 AGTWSTWSPWAMGTPSTGTIPKEIPAWGOLHTQPEVQVDSPPAPPRPSLQPHRLLDHR 360

QY 361 DSVEQVAVLASGLISFLGLVAGALALGLWLRRLRGKDGSKPGCFILASVIPDRRFGAP 420
DB 361 DSVEQVAVLASGLISFLGLVAGALALGLWLRRLRGKDGSKPGCFILASVIPDRRFGAP 420

QY 421 NL 422
DB 421 NL 422

RESULT 2
Q64385 ID Q64385 PRELIMINARY; PRT; 432 AA.
AC Q64385;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Interleukin-11 receptor ALPHA chain 1 precursor (NR1) (ETL2)
DE (IL-11RALPHA) (IL11RAL).
GN IL11RAL OR IL11RA OR ETL2 OR ETL2/IL11 REC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6 X CBA; TISSUE=LIVER;
RX MEDLINE=95045367; PubMed=7957045;
RA Hilton D.J., Hilton A.A., Raicevic A., Rakar S., Harrison-Smith M.,
RA Gough N.M., Begley C.G., Metcalf D., Nicola N.A., Willson T.A.;
RA "Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130
```

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RT for high affinity binding and signal transduction."
RN EMBO J. 13:4765-4775(1994).
[2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6; TISSUE=EMBRYO;
RA Neuhaus H., Bettenhausen B., Bilinski P., Simon-Chazottes D.,
RA Guenet J.L., Gossler A.;
RA Dev. Biol. 166:521-542(1994).
[3]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C, AND C57BL/6;
RA Gossler A.;
RA Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
[4]
RP SEQUENCE FROM N.A.
RX MEDLINE=97129000; PubMed=8973540;
RA Bilinski P., Hall M.A., Neuhaus H., Gissel C., Heath J.K., Gossler A.;
RT "Two differentially expressed interleukin-11 receptor genes in the
RT mouse genome."
RL Biochem. J. 320:359-363(1996).
[5]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11. BINDS TO IL-11
CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL.
CC -1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: WIDELY EXPRESSED.
CC -1- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. CONTAINS
CC ONE IG-LIKE DOMAIN.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
DR EMBL; X74953; CAA52908.1; -.
DR EMBL; U14412; AAA53248.1; -.
DR EMBL; X94162; CAA63873.1; -.
DR EMBL; X94163; CAA63873.1; JOINED.
DR EMBL; BC004619; AA04619.1; -.
DR HSP; P16471; Ibp3.
DR MGD; MGI-107426; Il11ral.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00041; fn3; 2.
DR Pfam; PF00047; fn3; 1.
DR SMART; SM00060; FN3; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 23 POTENTIAL.
FT CHAIN 24 432 INTERLEUKIN-11 RECEPTOR ALPHA CHAIN 1.
FT DOMAIN 24 367 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 368 393 POTENTIAL.
FT DOMAIN 394 432 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 41 102 IG-LIKE C2-TYPE DOMAIN.
FT CARBOHYD 127 127 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 194 194 N-LINKED (GLCNAC...) (POTENTIAL).
SQ SEQUENCE 432 AA; 46655 MW; 068389943502BBFC CRC64;

Query Match 83.4%; Score 1897; DB 11; Length 432;
Best Local Similarity 83.5%; Pred. No. 1e-137;
Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1;

QY 1 MSSSCSGLSRVLAVALVATVSVASSPCQAWGPPGVQYQGPGRSVKLCPCPGVTAGDPVSWF 60
DB 1 MSSSCSGLTRVLAVALVATVSVSSSPCQAWGPPGVQYQGPGRVYMLCCPGVSACTPVSWF 60

QY 61 RDGPKLLQGDPSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVYVSC 120
DB 61 RDGSRLLQGDPSGLGHELVLAQVDSDEGTYICQTLDGSGGMYTLKLGFPFPPARPEVSC 120

QY 121 QAADYENFSCWSPQSGLTRVLTYSRKTKVILGADSORSPSTGMPWPCQDPPLGAARC 180
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Db	121	QAVDIYENFCSWPGVSGUPLTIRLYTSYRKTKLPGAESQRESPTGMPCPDPLEASRC	180
Qy	181	VVHGAEEFWSQYRINVTEVNPGLASTRLLDVSLQSIILRDPDPQGLRVESVPGYPRRLRASW	240
Db	181	VVHGAEEFWSYRINVTEVNPGLASTCLLDVLRQLQSIILRDPDPQGLRVESVPGYPRRLHASW	240
Qy	241	TYPASWPCQPHFLKFLQRYRPAQHAWSTVEPAGLEEVIITDAVAGLPHAVRVVSARDFLD	300
Db	241	TYPASWRCQPHFLKFLQRYRPAQHAWSTVEPIGLEEVIITDAVAGLPHAVRVVSARDFLD	300
Qy	301	AGTWSWTSPEAWGTPSTGTIPKEIPAWGQLHTQ--PEVEPQVDSAPPAPPSLOPHRLLD	358
Db	301	AGTWSAWSPAWGTPSTGTPQLDDIPWSOGHQOQLAEVVAQEDSPAPAPPSLOPDRPLD	360
Qy	359	HRDSVEQVAVLASLGILSFLGLVAGALALGLWLRRLRGKDGSPKPGFLASVIPPVDRRPG	418
Db	361	HRDPLEQVAVLASLGIFSCGLGLAVGALALGLWLRRLRSKDGSPKPGGLLAPWIPVEKLPG	420
Qy	419	APNL 422	
Db	421	IPNL 424	
RESULT 3			
P70225			
ID	P70225	PRELIMINARY;	PRT; 432 AA.
AC	P70225; O09074;		
DT	01-FEB-1997 (TrEMBLrel. 02, Created)		
DT	01-FEB-1997 (TrEMBLrel. 02, Last sequence update)		
DT	01-MAR-2002 (TrEMBLrel. 20, Last annotation update)		
DE	Interleukin-11 receptor alpha chain 2 precursor (IL11RA2) (IL-11RBETA)		
DE	(Interleukin-11 receptor alpha chain 2 precursor (IL11RA2) (IL-11RBETA)		
GN	IL11RA2 OR IL-11RBETA.		
OS	Mus musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CD1; TISSUE=TESTIS;		
RX	MEDLINE=97129000; PubMed=8973540;		
RA	Billinski P., Hall M.A., Neuhans H., Gissel C., Heath J.K., Gossler A.;		
RT	"Two differentially expressed interleukin-11 receptor genes in the		
RT	mouse genome.";		
RL	Biochem. J. 320:359-363(1996).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CD-1; TISSUE=TESTIS;		
RX	MEDLINE=96278810; PubMed=8662802;		
RA	Robb L., Hilton D.J., Willson T.A., Begley C.G.;		
RT	"Structural analysis of the gene encoding the murine interleukin-11		
RT	receptor alpha-chain and a related locus.";		
RL	J. Biol. Chem. 271:13754-13761(1996).		
RN	[3]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=CD-1; TISSUE=TESTIS;		
RX	MEDLINE=97230451; PubMed=9073505;		
RA	Robb L., Hilton D.J., Brook-Carter P.T., Begley C.G.;		
RT	"Identification of a second murine interleukin-11 receptor alpha-chain		
RT	gene (IL11RA2) with a restricted pattern of expression.";		
RL	Genomics 40:387-394(1997).		
CC	-1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 11.		
CC	-1- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.		
CC	-1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.		
CC	-1- TISSUE SPECIFICITY: WIDELY EXPRESSED.		
DR	EMBL; X94157; CAA63872.1;		
DR	EMBL; X94158; CAA63872.1; JOINED.		
DR	EMBL; X94159; CAA63872.1; JOINED.		
DR	EMBL; X94160; CAA63872.1; JOINED.		
DR	EMBL; X94161; CAA63872.1; JOINED.		
DR	EMBL; X98519; CAA67144.1;		
DR	EMBL; U69491; AAC53114.1;		

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OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY;
RA Li R., Hartley L., Robb L.;
RT "Expression of interleukin-11 and interleukin-11 receptor alpha chain
in the rat uterus in the peri-implantation period.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF347936; AAK29624.1;
DR HSSP: P16471; 1BP3
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003530; Hemtopoptn_L_F3.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003600; Ig_Like.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00060; FN3; 2.
DR SMART: SM00409; IG; 1.
DR SMART: SM00410; IG_Like; 1.
DR PROSITE: PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 431 AA; 46784 MW; E086FD6B1688180B CRC64;

Query Match 81.8%; Score 1860.5; DB 11; Length 431;
Best Local Similarity 82.0%; Pred. No. 6.3e-135;
Matches 347; Conservative 21; Mismatches 54; Indels 1; Gaps 1;

QY 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPGVQYQVQGRSVKLCPCGVTAGDPVSWF 60
DB 1 MSSRSGLTRVLVAVATALVSSTPCQAWGPGVQYQVQGRPVMLCCPGVNAAGTPVSWF 60
QY 61 RDGPKLLQPDGSLGHELVLAQADSTDEGTYTCQLDGLGALGTVLQGLYPPARPVSC 120
DB 61 RDGDSRLQPDGSLGHELVLAQADSTDEGTYTCQLDGLGALGTVLQGLYPPARPVSC 120
QY 121 QAADYENFSCWTSPQISGLPTRYLTSYRKTKVLGADSRQSPSTGWPCQDPPLGAARC 180
DB 121 QAVDYENFSCWTSPQISGLPTRYLTSYRKTKVLGADSRQSPSTGWPCQDPPLGAARC 180
QY 181 VVHGAEPWSYRINVTNPLGASTRLLDVLSQILRPDPQGLRVESVPGYPRRLRASW 240
DB 181 VVHGAEPWSYRINVTNPLGASTRLLDVLSQILRPDPQGLRVESVPGYPRRLHASW 240
QY 241 TYPASWPCQPHLLKFRLOYRPAQHPAWSTVEPAGLEEVITDVAAGLPHAVRVSAEDFLD 300
DB 241 TYPASWRRQPHLLKFRLOYRPAQHPAWSTVEPIGLEELITDVAAGLPHAVRVSAEDFLD 300
QY 301 AGTWSWSPAWGTPSTGTIPKEIPAWQLHTQP-EVEPQVDSPPAPRPSLOPHPRLLDH 359
DB 301 AGTWSWSPAWGTPSTGTIPKEIPAWQLHTQP-EVEPQVDSPPAPRPSLOPHPRLLDH 359
QY 360 RDSVEQVAVLASIGLISFLGLVAGALALGWLRLRGKDGSPKPGFLASVIVDRRPGA 419
DB 361 RDPLEQVAVLASIGLISFLGLVAGALALGWLRLRRSGKDGSPKPGFLADMPIDKPLPGI 420
QY 420 PNL 422
DB 421 PNL 423

RESULT 5
O88507 PRELIMINARY; PRT; 372 AA.
AC O88507;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Ciliary neurotrophic factor receptor alpha precursor.
GN CNTFR.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Maeda M., Yaguchi N., Hanyuu C., Nakata Y., Onoda N., Tulin E.E.,
RT "Mouse homolog of human ciliary neurotrophic factor receptor.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF086615; AAC25711.1;
DR MGD; MGI:99605; Cntfr.
DR InterPro: IPR002996; CRIA.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR003530; Hemtopoptn_L_F3.
DR InterPro: IPR003598; Ig_c2.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00041; fn3; 1.
DR Pfam: PF00047; ig; 1.
DR SMART: SM00060; FN3; 1.
DR SMART: SM00408; IGC2; 1.
DR PROSITE: PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.
KW Immunoglobulin domain; Receptor; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 336 CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT ALPHA.
SQ SEQUENCE 372 AA; 40831 MW; EB75A9EE6A1BB8C8 CRC64;

Query Match 17.2%; Score 391; DB 11; Length 372;
Best Local Similarity 31.8%; Pred. No. 3.9e-22;
Matches 113; Conservative 49; Mismatches 163; Indels 30; Gaps 12;

QY 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPGVQYQVQGRSVKLCPCGVTAGDPVSWF 60
DB 1 MTASVPWACAVLAATAAAVYTKHSPQE--APHVQYERLGADVTLPCTASNDAAVTWR 58
QY 61 RDGPKLLQPDGSLGHELVLAQADSTDEGTYTCQLDGLG-ALGCTVTQLQGYPPARPVVS 119
DB 59 VNGCTD--LAPDLLNGSLILRSLELHSLGSLYACFHRDSWHLRHQVLLHVLPPREPVL 115
QY 120 QCAADY-ENFSCWTSFQISGLPT-RYLTSYRKTKVLGADSRQSPSTGWPCQDPPLGA 177
DB 116 CRSTNYPKGYCFSWH-----LPTPTIYIPNTFNVTNLHGSK-----IMVCEKDPALK 161
QY 178 ARCWHGAEPWS--QYRINVTNPLGASTRLLDVLSQILRPDPQGLRVESVPGYPRR 235
DB 162 NRCHIRYMLHLSFKIKYKVSISVSNALGHNTATTFDEFTIVKDPDENVVARVPSNPR 221
QY 236 LRASWTYPASWPCQPHLLKFRLOYRPAQHPAWSTVEPA-GLEEVITDVAAGLPHAVRV 294
DB 222 LEVTWQTPSTWPDSPESFPLKFFLRYRPLLDQWQHVLSGDTAHTTIDAYAGKEYIIQVA 281
QY 295 ARDFLDAGTWSWSPAWGTPSTGTIPKEIPAWQLHTQPEVQVDSPPAPRPS 349
DB 282 AKD-NEIGTWSWDSVAHAATPTEE-PRHLTTEAQ---APETTTSTTSSLAPPPT 331

RESULT 6
O35228 PRELIMINARY; PRT; 228 AA.
AC O35228;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Cytokine receptor-like molecule (Epstein-Barr virus induced gene
DE 3).
GN EB13 OR EB13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Nomura H., Yaguchi N., Hanyuu C., Maeda M., Kikuchi Y., Nakata Y.,
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[illegible]

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Db 66 YR----LGMARGHS-----WPCLOQTPTSTCITDQVLFSPAPYVLNVAVHPWGSS 116
QY 206 RLDDVSLQILRPPPOGLRVPESVPGYPRRLRASWTVPASWPCPHFLKFLKRYRPAQH 265
Db 117 SFVFPTEHIIKPPPEGVRLS--PLAERHVQVQWVEPPGWPFFEIFSLKWIYRIKQGA 174
QY 266 PAWSTVEFAGLEEVITDAVAGLPHA---VRYSDARDFDAGTWTWSPSEAMGTPTSG 318
Db 175 ARPHRVGPIEATSFILRAVR--PRARYVQVAAQDLTDYGELSDWSLPAATMSLG 228

RESULT 9
O57519 PRELIMINARY; PRT; 881 AA.
AC O57519;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Gp130p1.
GN XGP130.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Chen J., Grace A., Chien K.R.;
RT "Partial characterization of putative Xenopus gpl30.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF041845; AAC03531.1; -.
DR HSSP; P40189; IBOU.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR003529; Hemtopopn_L_F2.
DR Pfam; PF00041; fn3; 4.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS01353; HEMATOPO_REC_L_F2; UNKNOWN.1.
SQ SEQUENCE 881 AA; 99003 MW; 7DE7942D2D1138A0 CRC64;

Query Match 9.5%; Score 215.5; DB 13; Length 881;
Best Local Similarity 23.3%; Pred. No. 3.3e-08;
Matches 88; Conservative 61; Mismatches 145; Indels 83; Gaps 19;

QY 1 MSSCSGLRVLVAVATALYSASSPCQAWGPGVQVGPGRSVKLCPCGVTA---GDP 56
Db 5 ISFCLISSVVLIVHQELVKV---CGRIFFDPGIVHGERPFTA-YCVINQTCUREDASR 60
QY 57 VSWFRDG-----BPKLQGPDSGLGHELVLAQADSTDEGTICQTL-DGALGT---VT 106
Db 61 IYWLKGVKVPETQYEILNQTTSSVTEFL-----TTLNPLTCNVASGHVANTLYCIF 115
QY 107 LQLGYPARV-VSCQAADYENFSCWSPQISGLPTRYLTSYRKKTIVLGADSORRSPST 165
Db 116 FTGLGPDKPTNLTCIVYNODNLNLTCDWGRPTNLPTNYTLNLSH-WAHFGANYCRGANS 174
QY 166 GPWPCPDPLGAARCVH--GAEPWSOYRINVTVEVPLG-ASTRLDVSLSQILRPDPQ 222
Db 175 -----CTHSPGFQYIITTCQVEATNEIGIKSTLTDVNVKPNPQ 220
QY 223 GLRVESVPGYPRRLRASWTVPASWPCPHFLKFLKRYRPAQHPAWSTV-----EP 273
Db 221 LSELISLELPNALKIEWKNPIT---NAENLKNYIRYRPVKTDWEMVPEEDTASHRDS 276
QY 274 AGLEEVITDAVAGLPHAVRSARDFLDAGTWTWSPSEAMGTPTSGTIPKEIPA 326
Db 277 FTLODLLPNTYEV--SIRCIHKD--GHGFWSDWSELKQVTPDEA--PPSRG----- 322
QY 327 WQLHTOPEVEPOVDS 343
Db 323 -----PDIWKKIDSP 332
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RESULT 10
O75462 PRELIMINARY; PRT; 422 AA.
AC O75462;
DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
DE Cytokine-like factor-1 precursor.
GN CLF-1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Elson G.C.A., Graber P., Losberger P., Herren S., Gretener D.,
RA Menoud L.N., Wells T.N.C., Kosco-Vilbois M.H., Gauchat J.F.;
RT "CLF-1, a Novel Soluble Protein Shares Homology With Members of the
RT Cytokine Type-I Receptor Family.";
RL J. Immunol. 0:0-0(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Magrangeas F., Jacques Y., Minvielle S.;
RT "Cloning and expression of a novel soluble protein containing
RT hemopoietic cytokine receptor domains.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF059293; AAC28335.1; -.
DR EMBL; AF073515; AAD39681.1; -.
DR HSSP; PF6471; 1BP3.
DR InterPro; IPR002996; CR1A.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR Receptor; Signal.
FT SIGNAL 1 37 POTENTIAL.
FT CHAIN 38 422 CYTOKINE-LIKE FACTOR-1.
SQ SEQUENCE 422 AA; 46301 MW; AD9DEFB01B84228 CRC64;

Query Match 9.3%; Score 211.5; DB 4; Length 422;
Best Local Similarity 23.7%; Pred. No. 2.7e-08;
Matches 91; Conservative 53; Mismatches 145; Indels 95; Gaps 19;

QY 7 GLSRVLVAVATALYSASSPCQAWGPGVQVGPGRSVKLC-----PGVTAGDPVSWF 60
Db 30 GAPRAGSGAHTAVISPODPTILLI-----GSSLLATCSVHGDPGATA-EGLYWT 77
QY 61 RDGE---PKLQGPDSGLGHELVLAQAD-----STDEGTICQTLDGALGTVTLQIGYP 112
Db 78 LNGRRLPPELSRVNLAS---TLALALANLNGSRQSRGDLNVLCHARDGSIAGSLYVGLP 134
QY 113 PARPV-VSCQAADYENFSCWSPSQ--ISGLPTRYLTSYRKKTIVLGADSORRSPSTGWP 169
Db 135 PERPVNTSCSKNMKDLTCRWTPGAHGETFLHTNYSKYLRWYQDNTCEEYHTVGPHS 194
QY 170 C--PODPLGAARCVHGAEPWSOYRINVTVEVPLG-ASTRLDVSLSQILRPDPQGLRV 226
Db 195 CHPKD-----LALFTPEIWEATNRLGARSVDVLILDVTTDPPDVHV 243
QY 227 ESVPGYPRRLRASWTVPASWPCPHFL--KFRLOYRPAQHPAWSTVEP-----AG 275
Db 244 SRVGLEDQLSVRWSP---PALKDFLFOAKYQIRYVEDSDVKVVDVSNQTSCLRAG 300
QY 276 LEEVITDAVAGLPHAVRSARDF-----LDAGTWTWSP-PEA----- 311
Db 301 LK-----PCTVYFQVQRCNPFGIYKSKAGINSEWSHPTAASTPRSRPGGGACEP 353
QY 312 -WGTPSTGTIPKEIP---AWGQLH 331
Db 354 RGGEPSGVPVRELKQFLGWLKH 377

RESULT 11
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Q9UHH5
ID Q9UHH5 PRELIMINARY; PRT; 422 AA.
AC Q9UHH5;
DT 01-MAY-2000 (TremBLrel. 13, Created)
DT 01-MAY-2000 (TremBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Class I cytokine receptor.
GN ZCYTOR5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Lok S., Presnell S.R., Jelmsberg A.C., Gilbert T., Whitmore T.E.,
RA Foster D.C., Adams R.L., Lehner J.M., O'Hara P.J.;
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF178684; AAD54385.1; -.
DR HSSP; PI6471; 1BP3.
DR InterPro; IPR002996; CR1A.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
KW Receptor.
SQ SEQUENCE 422 AA; 46315 MW; 0D2C5F7A01B942EE CRC64;

Query Match 9.3%; Score 210.5; DB 4; Length 422;
Best Local Similarity 23.7%; Pred. No. 3.3e-08;
Matches 91; Conservative 53; Mismatches 145; Indels 95; Gaps 19;

QY 7 GLSRVLVAVATALVSASSPCQAWGPPGVQYQPGRSVKLCC-----PGVTAGDPVSWF 60
DB 30 GAPRAGSGAHTAVISQDPDTLLI-----GSSLATCSVHGDPGATA-EGLYWT 77
QY 61 RDGE---PKLQGPSGLGHELVLAQAD-----STDEGTYICQTLGALGGTVTLQGY 112
DB 78 LNGRLPPELSRVLNAS---TLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLP 134
QY 113 PARPV-VSCQAADYENFSCWSPSQ--ISGLPTRYLTYSRKKTVLGADSORSPSTGWP 169
DB 135 PEKPNVNSCWSKMKDLCTRWTPGAHGETFLHTNYSKYKLEWYQDNTCEEYHVGPHS 194
QY 170 C--PODPLGAACVYVHGAFFWSQYRINTVEVNPGLG-ASTRLDLVLSQSLRPPQGLRV 226
DB 195 CHIPKD-----LALFTPEIWEATNRLGARSVDLTLDLDVVTTPDPPEVHV 243
QY 227 ESVPYPRRLRASWTYPASWPCQPHLL--KFLQYRPAQHPAWSTVEP-----AG 275
DB 244 SRVGGLEDQLSVRWVSP---PALKDFLQAKYQIRYVEDSDVKVDDVSNQTSCLAG 300
QY 276 LEEVITDAVAGLPHAVRYSARDF-----LDAGTWSTWS-PEA----- 311
DB 301 LK-----PGTVFYVQVRCNPFGIYGSKKAGIWEWSHPTAASPRSRPCGGGACEP 353
QY 312 -WGTPSTGTIPEIP---AWGQLH 331
DB 354 RGGEPSGPGVRRELKQFLGWLKKH 377

RESULT 12
Q9JMS8
ID Q9JMS8 PRELIMINARY; PRT; 425 AA.
AC Q9JMS8;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2002 (TremBLrel. 20, Last annotation update)
DE Cytokine receptor like molecule 3 precursor.
GN CRLF1 OR CRLF3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
```

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RP SEQUENCE FROM N.A.
RA Hiroyama T., Iwama A., Nakamura Y., Nakauchi H.;
RT "cytokine receptor like molecule 3.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB040038; BAA92777.1; -.
DR HSSP; PI6471; 1BP3.
DR MGD; MGI:1340030; Cr1f1.
DR InterPro; IPR002996; CR1A.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 1.
KW Receptor; Signal.
FT SIGNAL 1 34 POTENTIAL.
SQ SEQUENCE 425 AA; 46662 MW; 910535C629CA7056 CRC64;

Query Match 9.2%; Score 209.5; DB 11; Length 425;
Best Local Similarity 23.9%; Pred. No. 3.9e-08;
Matches 89; Conservative 53; Mismatches 138; Indels 93; Gaps 18;

QY 17 TALVSASSPCQAWGPPGVQYQPGRSVKLCC-----PGVTAGDPVSWFRDGEKLLQG 70
DB 43 TAVISQDPDTLLI-----GSSLQATCSIHGDTFGATA-EGLYWTNG--RRLPS 88
QY 71 PDSGLGHELVLAQADSTDEGT-----YICQTLDELGGTVTLQGYPPARPV-VSCQA 122
DB 89 ELSRLNTSTLALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEKPNISCSW 148
QY 123 ADYENFSCWSPSQ--ISGLPTRYLTYSRKKTVLGADSORSPSTGWPCC--PQDPLGNA 178
DB 149 RNMKDLCTRWTPGAHGETFLHTNYSKYKLEWYQDNTCEEYHVGPHSCHLIPKD----- 203
QY 179 RCVHGCAFWSQYRINTVEVNPGLG-ASTRLDLVLSQSLRPPQGLRVESVPGYPRRLR 237
DB 204 -----LALFTPEIWEATNRLGARSVDLTLDLDVVTTPDPDVHVRVGGLEDQLS 257
QY 238 ASWTYPASWPCQPHLL--KFLQYRPAQHPAWSTVEP-----AGLEEVIITDAVAG 286
DB 258 VRWVSP---PALKDFLQAKYQIRYVEDSDVKVDDVSNQTSCLAGLK-----PG 307
QY 287 LPHAVRYSARDF-----LDAGTWSTWS-PEA-----WGTPSTGTIP 321
DB 308 TVIFYVQVRCNPFGIYGSKKAGIWEWSHPTAASPRSRPCGGGVCPRGEGSSGPVR 367
QY 322 KEIP---AWGQLH 331
DB 368 RELKQFLGWLKKH 380

RESULT 13
Q9GLW3
ID Q9GLW3 PRELIMINARY; PRT; 227 AA.
AC Q9GLW3;
DT 01-MAR-2001 (TremBLrel. 16, Created)
DT 01-MAR-2001 (TremBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)
DE Prolactin receptor (Fragment).
OS Ursus maritimus (Polar bear) (Thalarcos maritimus).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ursus.
OX NCBI_TaxID=29073;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LIVER;
RX MEDLINE=20086658; PubMed=10618652;
RA Howell-Skalla L.A., Bunick D., Bleck G.T., Nelson R.A., Bahr J.M.;
RT "Cloning and sequence analysis of the extracellular region of the
RT polar bear (Ursus maritimus) luteinizing hormone receptor (LHR),
RT follicle stimulating hormone receptor (FSHR), and prolactin receptor
RT (PRLr) genes and their expression in the testis of the black bear
RT (Ursus americanus)".
RL Mol. Reprod. Dev. 55:136-145(2000).
DR EMBL; AF169792; AAG10648.1; -.
DR HSSP; PI4787; IAN3.
```

Qy	64	EPKLLQDPSGLGHELVLAQADSTDEGTYIC-----QTL-----DGLGGTVTLQ 109
Db	65	SSEVL-----GSGKTLILVKFEFDAGHYTCHRGGEVLSQMLLLHKNEDGIWSTDILKK 119
Qy	110	GYPARPVWVSCAADYE-NFSCWTSWPSQISGLPTRYLTYSRKTYVLGADSORRSPSTGWP 168
Db	120	KEPENKMLVTCFAKNYSGRFTCMW-----LTAISTDVKFVKSHRGSSDPQGV 167
Qy	169	PCPDPLGAARCVVHGAEFWSQRYINVTENVPLGASTRLLDVS----- 211
Db	168	TCGATLSAERVKTEQREY-KKYSVQCOEDNACPTAETLPIVVDVAVHKLKYENWIS 226
Qy	212	--LQSLRPPDPOGLRVSEVPGYPRRLRASWTYPASWPCOPH--FLIKFRLQYRPAQHFA 267
Db	227	FFIRDIKDPDPKMLKMKP-SKTPQQQVEVTWEYPDW-SITPHYSFSLTFSVQVQGGKKKR 284
Qy	268	WSTVEPAGLEIVTDVAGLPHAVRSARDFLDAGTWSTWS 308
Db	285	SNTLH---VDKTSVTVCQKGAKVSVQARDRYNNSWSEWA 322
RESULT 15		
ID	Q16354	PRELIMINARY; PRT; 206 AA.
AC	Q16354;	
DT	01-NOV-1996 (TEMBLrel. 01, Created)	
DT	01-NOV-1996 (TEMBLrel. 01, Last sequence update)	
DT	01-MAR-2002 (TEMBLrel. 20, Last annotation update)	
DE	Prolactin receptor (Fragment).	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	MEDLINE=95286597; PubMed=7768908;	
RT	Fuh G, Wells J.A.;	
RA	"Prolactin receptor antagonists that inhibit the growth of breast	
RT	cancer cell lines";	
RL	J. Biol. Chem. 270:13133-13137(1995).	
DR	EMBL; S78505; AAB34470.1; -	
DR	HSSP; P16471; 1BP3.	
DR	InterPro; IPR002996; CRIA.	
DR	InterPro; IPR003961; FN.III	
DR	InterPro; IPR003328; Hemtopoptn_L.Fl.	
DR	Pfam; PF00041; In3; 2.	
DR	SMART; SM0060; FN3; 1.	
DR	PROSITE; PS01352; HEMATOPO_REC_L.Fl; UNKNOWN_1.	
KW	Receptor.	
FT	NON_TER.	
FT	SEQUENCE 206 AA; 23950 MW; CED939781B3C804E CRC64;	
Query Match 8.4%; Score 190.5; DB 4; Length 206;		
Best Local Similarity 27.8%; Pred. No. 4.7e-07;		
Matches 62; Conservative 27; Mismatches 93; Indels 41; Gaps		
Qy	112	PPARP-VVSCAADYENFSCWTSWPSQISGLPTRYLTYSRKTYVLGADSORRSPSTGWP 170
Db	3	PPGPEIFKCRSPNKETFTCWWRPGTGGGLPTYSLT-----HREGETLMHEC 51
Qy	171	PDPLGAARCVVHGAEF--WSQRYINVTENVPLGAS--TLLDVSLSQSLRDPDPOGLRV 226
Db	52	PDYITGGPNSCHFGKQYTSWRYIIMVNATNMGSSFSDLEYVDVYIVQDPDPLELV 111
Qy	227	ESVEGYPRR--LRASWTYP-----ASWPCQPHLLKFLRLQYRPAQHAWSTVEPAS--L 276
Db	112	EVKQPEDRKPYLWIKNSPPTLIDLTGW-----FTLLYEIRLKPRAAEWE-IHPAQGT 165
Qy	277	EEVITDVAAGLPHAVRSARDFLDAGTWSTWS-----PEAW 312
Db	166	EFKTSLSLHPQKYLQVQRCKP--DHGYVWSAWSAPATTIQIPSAW 206

Sat Jan 18 21:53:46 2003

us-09-924-338-2.rspt

Page 9

Search completed: January 17, 2003, 19:39:09
Job time : 45 secs

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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:35:38 ; Search time 14 Seconds
(without alignments)
1250.215 Million cell updates/sec

Title: US-09-924-338-2

Perfect score: 2275

Sequence: 1 MSSSCSLRVLAVATALV.....KPGFLASVIVDRRPGAPNL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	395.5	17.4	460	1 IL6A_MOUSE	P22272 mus musculus
2	392	17.2	372	1 CNTR_RAT	Q08406 rattus norv
3	390.5	17.2	462	1 IL6A_RAT	P22273 rattus norv
4	382	16.8	372	1 CNTR_HUMAN	P26992 homo sapien
5	381	16.7	362	1 CNTR_CHICK	P51641 gallus gall
6	360	15.8	468	1 IL6A_HUMAN	P08887 homo sapien
7	326.5	14.4	467	1 IL6A_PIG	O18796 sus scrofa
8	234	10.3	831	1 PRLR_MELGA	Q91094 meleagris g
9	221	9.7	830	1 PRLR_COLLI	Q90374 columba liv
10	214	9.4	831	1 PRLR_CHICK	O04594 gallus gall
11	209.5	9.2	581	1 PRLR_SHEEP	O46561 ovis aries
12	204.5	9.0	581	1 PRLR_BOVIN	Q28172 bos taurus
13	204	9.0	616	1 PRLR_RABIT	P14787 oryctolagus
14	197.5	8.7	581	1 PRLR_CEREL	Q28235 cervus elap
15	190	8.4	327	1 IL2B_MARMO	Q61729 marmota mon
16	190	8.4	327	1 IL2B_SHEEP	O02815 ovis aries
17	189	8.3	622	1 PRLR_HUMAN	P16471 homo sapien
18	186	8.2	1266	1 NCRA_CHICK	Q03696 gallus gall
19	184	8.1	327	1 IL2B_BOVIN	P46282 bos taurus
20	183	8.0	327	1 IL2B_CEREL	Q28234 cervus elap
21	183	8.0	610	1 PRLR_RAT	P05710 rattus norv
22	174.5	7.7	324	1 IL2B_PIG	Q28938 sus scrofa
23	174.5	7.7	329	1 IL2B_FELCA	O02744 felis silve
24	174	7.6	608	1 PRLR_MOUSE	Q08501 mus musculus
25	173.5	7.6	630	1 PRLR_ORENI	Q91513 oreochromis
26	167.5	7.4	328	1 IL2B_HUMAN	P29460 homo sapien
27	166.5	7.3	761	1 NCRA2_HUMAN	P13592 homo sapien
28	164.5	7.2	328	1 IL2B_MACMU	P48095 macaca mula
29	164	7.2	329	1 IL2B_HORSE	Q9XSD5 equus cabal
30	150	6.6	918	1 IL6B_HUMAN	P40189 homo sapien
31	149.5	6.6	853	1 NCAL_BOVIN	P31836 bos taurus
32	148.5	6.5	329	1 IL2B_CANFA	Q28268 canis famil
33	148	6.5	335	1 IL2B_MOUSE	P43432 mus musculus

ALIGNMENTS

RESULT 1

ID	IL6A_MOUSE	STANDARD;	PRT;	460 AA.
AC	P22272;			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1992 (Rel. 23, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1).			
GN	IL6RA OR IL6R.			
OS	Mus musculus (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID=10090;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=BAIB/C; TISSUE=Spleen;			
RX	MEDLINE=90278354; PubMed=2112585;			
RA	Sugita T., Totsuka T., Saito M., Yamasaki K., Taga T., Hirano T., Kishimoto T.;			
RT	"Functional murine interleukin 6 receptor with the intracisternal A particle gene product at its cytoplasmic domain. Its possible role in plasmacytomagenesis";			
RT	J. Exp. Med. 171:2001-2009(1990).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=C3H; TISSUE=Liver;			
RA	Fiorillo M.T., Ciliberto G., Dente L.;			
RL	Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE REACTIONS AND HEMATOPOIESIS.			
CC	-!- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-!- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.			
CC	-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC	-!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.			
CC	-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC	-----			
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CC	-----			
DR	EMBL; X51975; CAA36237.1; -			
DR	EMBL; X53802; CAA37810.1; -			
DR	PIR; J01144; J01144.			
DR	PIR; J01145; J01145.			
DR	PIR; S14543; S14543.			
DR	HSSP; P16471; 1BP3.			

P46658 cercocebus
P13596 rattus norv
P13591 homo sapien
Q99062 homo sapien
Q9QZS7 mus musculus
Q9R044 rattus norv
P10586 homo sapien
Q00560 mus musculus
P43703 mus musculus
P48356 mus musculus
P42702 homo sapien
P16882 mus musculus

```

DR MGD; MGI:105304; Il6ra.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003530; Hemtopoptn_L_F3.
DR InterPro; IPR003006; Ig_MHC.
DR InterPro; IPR003598; Ig_c2.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW Receptor; Transmembrane; Immunoglobulin domain; Repeat;
KW Signal.
FT CHAIN 1 19 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
FT DOMAIN 20 460 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 20 364 POTENTIAL.
FT DOMAIN 365 385 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 386 460 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 40 99 BY SIMILARITY.
FT DISULFID 25 190 BY SIMILARITY.
FT DISULFID 47 92 BY SIMILARITY.
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 162 173 BY SIMILARITY.
FT CARBOHYD 32 32 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 374 374 A -> R (IN REF. 2).
SQ SEQUENCE 460 AA; 50454 MW; F85C5906D08525C4 CRC64;

Query Match 17.48; Score 395.5; DB 1; Length 460;
Best Local Similarity 30.78; Pred. No. 2.4e-20;
Matches 145; Conservative 58; Mismatches 178; Indels 91; Gaps 25;

QY 1 MSSCSGLSRVLAVATVALVSASSPCQAMGPPGVQYQGKRSVKLCPCGYTAGDPVS-- 58
Db 2 LTGCTLLVALLAAPVALVLGS--CRALEVANGTVISLPATVTLICPGKEAGNVTIH 59
QY 59 WFRGEPKLLGQPD-SGLGHELVLAQADSTDEGYICQTLGALGGVTVLQGLYPPARPV 117
Db 60 WYSGS-----QNREWTITGNTLVLRDVLQSDTGDYLC-SLNDHLVGVTVPLLDVDPPEPK 114
QY 118 VSC-QAADYENFSCWSPSOISGLPTRYLTYSRKTKVLGADSORSPSTGWPQCP-QDPL 175
Db 115 LSCFRKPNLVNAICEWRFSSTPS-PTTKAVLVFAKKI-----NTNGKSDFOVPCQYSQQL 168
QY 176 GAARCVVHGAEEFWSOYRI-NVTEYNPLGASTRLDDV--SLQSLRPDPPOGLRVESVPGY 232
Db 169 KSFSCQVEILEGDKVYHIVSLCVANSVSGKSSHNEAFSLK-WQPDPPANLVSAIPGR 227
QY 233 PRLRLASWTYPASWPCOPHFLKFLRLOYRPAQHAPWS-----TVEPAGLEEVITDAVAG 286
Db 228 PRLWKVSNQHPETWD-PSYLLQLQRLRYR-----PWWSKEFTVLLLPVAQYQCVIHDALRG 282
QY 287 LPHAVRVYSARDFLDAGTWSTWSPAWGTPTSGTIPKEIPA---WGQLHTQPEVEPQVDS 343
Db 283 VKHVQVVRGKEELDGLGWSESPVETGPIWAE-PRTPAGILMNP--TQVSVE---DS- 335
QY 344 APPRPSLOPHRLDHRD-----SVEQVAVLA-----SLGILSPGLVAGALALGLW--- 390
Db 336 -----ANHEDQVESSTEATSVLAPVQESSMSLPTFL-VAGSGFLGLLVCV 381
QY 391 ---LRLRGKGD-----GSPKPGFLASVIVDRRPGAPN 421
Db 382 FIILRLQKQKWEAEKESKTTSPPPPSYGLGPKLPTPLVPLLTTPHSSGSDN 433

RESULT 2
CNTR_RAT
ID CNTR_RAT STANDARD; PRT; 372 AA.
AC Q08406;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)

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DE OS Rattus norvegicus (Rat).
GN CNTRF.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=93152175; PubMed=8381290;
RA Ip N.Y., McClain J., Barrezaeta N.X., Aldrich T.H., Pan L., Li Y.,
RA Wiegand S.J., Friedman B., Davis S., Yancopoulos G.D.;
RT "The alpha component of the CNTRF receptor is required for signaling
RT and defines potential CNTRF targets in the adult and during
RT development."
RL Neuron 10:89-102(1993).
RN [2]
RP SEQUENCE OF 185-277 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=93211934; PubMed=8460125;
RA Clatterbuck R.E., Price D.L., Koliatsos V.E.;
RT "Ciliary neurotrophic factor prevents retrograde neuronal death in
RT the adult central nervous system."
RC Proc. Natl. Acad. Sci. U.S.A. 90:2222-2226(1993).
CC -!- FUNCTION: BINDS TO CNTRF (GPA). THE ALPHA CHAIN PROVIDES THE
CC RECEPTOR SPECIFICITY.
CC -!- SUBUNIT: HETEROPRIMER OF THE ALPHA CHAIN, LIFR AND GPI30.
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC -!- TISSUE SPECIFICITY: NERVOUS SYSTEM.
CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
EMBL; S54212; AAB25290.1; -
EMBL; S57711; AAB25918.1; -
PIR; A47387; A47387.
InterPro; IPR002996; CRIA.
InterPro; IPR003961; FN.III.
InterPro; IPR003530; Hemtopoptn_L_F3.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003598; Ig_c2.
Pfam; PF00041; fn3; 1.
Pfam; PF00047; Ig; 1.
SMART; SM00060; FN3; 1.
SMART; SM00408; IGC2; 1.
PROSITE; PS01354; HEMATOPO_REC_L_F3; 1.
KW Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.
FT SIGNAL 1 20 POTENTIAL.
FT CHAIN 21 342 CILIARY NEUROTROPHIC FACTOR RECEPTOR
FT ALPHA.
FT PROPEP 343 372 REMOVED IN MATURE FORM (POTENTIAL).
FT DOMAIN 39 96 IG-LIKE C2-TYPE DOMAIN.
FT DOMAIN 201 302 FIBRONECTIN TYPE-III.
FT DISULFID 46 89 POTENTIAL.
FT CARBOHYD 60 60 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 70 70 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 142 142 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT LIPID 342 342 GPI-ANCHOR (POTENTIAL).
FT CONFLICT 261 261 N -> D (IN REF. 2).
SQ SEQUENCE 372 AA; 40822 MW; 3B87EE63923FB149 CRC64;

```

Query Match 17.28; Score 392; DB 1; Length 372;
Best Local Similarity 31.9%; Pred. No. 3.2e-20;

Matches 113; Conservative 49; Mismatches 164; Indels 28; Gaps 12;

QY 1 MSSSCGSLRVAVATALVSASSPCQAWGPGVQYQGRSVKLCPCPGVTAGDPVSWF 60
 Db 1 MAASVPWACCAVLAANAATVQKHSPQE--APHVQYERLGTDTVPCGTASWDAAVTWR 58
 QY 61 RDGEFKLLQGGSLGHELVLAQADSTDEGTIYICQTLDG-ALGGTIVTLQGLYPPARPVYS 119
 Db 59 VNGTD---LAPDLNGSOLILRSLELGHSLGYACFHRDSWHLRHQVLLHVLGPPREPVL 115
 QY 120 COADY-ENFSCWSPSOISGLPRYLTSYRKVILGADSORRSPSTGFWPCQDPLGA 178
 Db 116 CRSNTPKGFYCSHLS---APT-YIPNTFNVTVLHGSKM-----MVCEKDPALKN 162
 QY 179 RCVVHGAEFWS--OYRINVTENVPLGASTRLLDVSLQSLRPDPPOGLRVESVPGPRRL 236
 Db 163 RCHRYMHLFTIKYKVISVSNALGHTNTAITDEFTIVRDPDPENVVAPVSPNPRRL 222
 QY 237 RASWTYPASWPCQPHFLKFLQYRPAQHPAWSTVEPA-GLVEVITDAVAGLPHAVRYS 295
 Db 223 EVTWQTPSTWDPESFPLKFLRYRPLLDQWQHVLSNGTAHTITDAYACKEXIIQVAA 282
 QY 296 RFDLDAGTWSTWSEANGCTPGTIPKEIPAWGQLHTQPEVDPQVDSAPPSPS 349
 Db 283 KD-NEIGTWSWDSVAHAATPWTEE-PRHLTTEAQ---APETTTSTTSSLAAPPPT 331

RESULT 3

IL6A_RAT STANDARD; PRT; 462 AA.

AC P22273;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1).
 GN IL6R.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fischer 344; TISSUE=Liver;
 RX MEDLINE=91060602; PubMed=2174054;
 RA Baumann M., Baumann H., Fey G.H.;
 RT "Molecular cloning, characterization and functional expression of the
 RT rat liver interleukin 6 receptor.";
 RL J. Biol. Chem. 265:19853-19862(1990).
 RN [2]
 RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.
 RA Gibson T.;
 RL Unpublished observations (FEB-1995).
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 CC WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL
 CC ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 CC LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 CC REACTIONS AND HEMATOPOIESIS.
 CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 CC C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL: M58587; AAA41431.1; -;
 DR PIR: A37986; A37986.
 DR HSSP: P16471; 1BP3.
 DR InterPro: IPR002996; CRIA.
 DR InterPro: IPR003961; FN_III.
 DR InterPro: IPR003530; Hemtopoptn_L_F3.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00047; Ig; 1.
 DR SMART: SM00060; FN3; 1.
 DR SMART: SM00408; IGC2; 1.
 DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
 DR Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 KW Signal.
 FT CHAIN 1 19
 FT DOMAIN 20 462
 FT TRANSMEM 20 364
 FT DOMAIN 365 385
 FT DOMAIN 386 462
 FT DOMAIN 40 99
 FT DISULFID 25 190
 FT DISULFID 47 92
 FT DISULFID 117 128
 FT DISULFID 162 173
 FT CARBOHYD 32 32
 FT CARBOHYD 55 55
 FT CARBOHYD 85 85
 FT CARBOHYD 150 150
 FT CONFLICT 227 261
 FT SLVGSKVGKTLSPGTQVTTCCNSFFDLYGQRT
 FT (IN REF.1).
 SQ SEQUENCE 462 AA; 50398 MW; 44D6064CEDC0537D CRC64;
 Query Match 17.2%; Score 390.5; DB 1; Length 462;
 Best Local Similarity 30.8%; Pred. No. 5.2e-20;
 Matches 144; Conservative 55; Mismatches 183; Indels 85; Gaps 25;

QY 1 MSSSCGSLRVAVATALVSASSPCQAWGPGVQYQGRSVKLCPCPGVTAGD--PVS 58
 Db 2 LAVGCTLLVALLAPAVALVLS--CRALEVANGVTSLPGATVTLICPKAAGNATH 59
 QY 59 WFDGEPLKLGPD--SGLGHELVLAQADSTDEGTIYICQTLDGALGSTVTLQGLYPPARPV 117
 Db 60 WYSGS-----OSREWTTTGTNTLVLRVAVQVNDTGHVLC-FLDDHLVGTVPLLVDPPEEPK 114
 QY 118 VSC-QAADYENFSCWSPSOISGLPRYLTSYRKVILGADSORRSPSTGFWPCP-QDPL 175
 Db 115 LSCFRKNPLVNACFCEHPSSTPS-PTTKAVMEAKI-----NTTNGKSDFOVPCQYSOOL 168
 QY 176 GAARCVVHGAEFWSQYRI-NVTEVNPGLGASTRLLDVSLQSI--LRDPDPQGLRVESVPGY 232
 Db 169 KSFSEVEILEGDKYVHIVSLCVANSVG--SRSSHNVVFQSLKMWQPPDPANLVWSAIPGX 227
 QY 233 PRRLRASWTYPASWPCQPHFLKFLQYRPAQHPAWS--TVEPAGLEE--VITDAVAG 286
 Db 228 PRWLKVSQWQDPESWD-PSYILLQFELRYR----PWSKXFTVWPLOVQAQHCVIIDALRG 282
 QY 287 LPHAVRVSARDFDAGTWSTWSEANGCTPGTIPKEIPAWGQLHTQPEVEPQVDSAPP 346
 Db 283 VKHVQVGRKEEFDIGQWSKWSPEVTGP-----W---LAERTTTAGTGNPT 328
 QY 347 RPSLQPHRLLDHRD-----SVEQAVLA-----SLGILSFLGLVAGALALGLW----- 390
 Db 329 QVSVEDYD---NHEDQYGSSTEATSVLAPVOGSSPIPLPTFL-VAGGSLAFGLLLCVFTI 384
 QY 391 LRLRGGKD-----GSPKPGFLASVIVDRPRGAPN 421
 Db 385 LRLKKKKWSQAEKESKSTSPPPYPLGLPKPTFL--LVPLLTSPGSHN 429

RESULT 4


```

Db 134 SLET-----KTSASTYLLAKWSPPLADVTSTNSHVYVYELRLKPEEKEWETVS-VGV 186
QY 277 EE--VITDAVAGLPHAVRVARSARDLFDAGTWTWSPEANGTSTGTIPKEIP 325
Db 187 QTQYKVNRLQAGVKYVQV--RCVLDIGEMSEWSSERHIHPNGESPPEKP 235

RESULT 10
PRLR_CHICK
ID PRLR_CHICK STANDARD; PRT; 831 AA.
AC Q04594;
RC STRAIN=White leghorn; TISSUE=Kidney;
RX MEDLINE=93075121; PubMed=1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
the cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 188:490-496(1992).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -----
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CC -----
DR EMBL: D13154; BAA02439.1; -.
DR PIR: JQ1655; JQ1655.
DR HSSP: P16471; 1BP3.
DR InterPro: IPR002996; CRI1.
DR InterPro: IPR003961; FN_III.
DR Pfam: PF00041; fn3; 4.
DR SMART: SM00060; FN3; 3.
DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.
FT SIGNAL 1 23
FT CHAIN 24 831
FT DOMAIN 24 438
FT TRANSMEM 439 459
FT DOMAIN 460 831
FT DOMAIN 25 122
FT DOMAIN 123 225
FT DOMAIN 228 325
FT DOMAIN 326 428
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 91 91
FT CARBOHYD 100 100
FT CARBOHYD 112 112
FT CARBOHYD 132 132
FT CARBOHYD 262 262
FT CARBOHYD 303 303
FT CARBOHYD 315 315

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FT CARBOHYD 335 335 N-LINKED (GLCNAC... ) (POTENTIAL).
SQ SEQUENCE 831 AA; 94102 MW; 1C4E75791DCADBE9 CRC64;

Query Match 9.4%; Score 214; DB 1; Length 831;
Best Local Similarity 27.5%; Pred. No. 1.6e-08;
Matches 76; Conservative 42; Mismatches 108; Indels 50; Gaps 15;

QY 113 PARP--VWSCQAADYENFSCWSPSOISGLPTRYLTSYRKKTVLGADSORRSPSTGFWPCP 171
Db 28 PCKKIIIRCSLEKETFSCKWKPGSDGGLPTNYTLFYSK-----DSEEEI-----YECF 76
QY 172 Q-DPLGAARCVV--HGAFFWQYRINVTENPLGAST---RLLDVSLQSIILRPDPPOGLR 225
Db 77 DYRTSGPNSCYFNKNHTSPWTTNTITATNEIGNSSDPQYVDVT--SIVQGGSPVNL 134
QY 226 VESVPGYPRR-----LRASWTYPASWPCQPHFLKFLRQYRPAQHPAWSIVEPAGLEE- 278
Db 135 LET-----KRSANIMYLWAKSPPLADASSNHLHYELRIKPEKEWETIS-VGVQTP 188
QY 279 -VITDAVAGLPHAVRVARSARDLFDAGTWTWSPEANGTSTGTIPKEIPAWGOLHTQPEVE 337
Db 189 CKINRLNAGMRVQV--RCTLDPGSEWSSERHILIPSGQSPPEKPTIIKCRS-PEKE 245
QY 338 -----PQVDSAPPSPRLPRLDHRDSVEQV 366
Db 246 TFTCWKPKGLDGGHPTNVT-----LLYSKEGEQV 275

RESULT 11
PRLR_SHEEP
ID PRLR_SHEEP STANDARD; PRT; 581 AA.
AC Q46561; P79205; Q46574; Q46573; P79203; Q46569;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (OPR).
GN PRLR.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Liver, and Mammary gland;
RX MEDLINE=98001468; PubMed=9343303;
RA Bignon C., Binard N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
and genomic analysis reveal that the two forms arise by different
alternative splicing mechanisms in ruminants and in rodents.";
RL J. Mol. Endocrinol. 19:109-120(1997).
RN [2]
RP SEQUENCE OF 61-395 FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
SPECIFICITY.
RC STRAIN=Scottish blackface; TISSUE=Anterior pituitary;
RX MEDLINE=99049302; PubMed=9832462;
RA Tortorese D.J., Brooks J., Ingleton P.M., McNeilly A.S.;
RT "Detection of prolactin receptor gene expression in the sheep
pituitary gland and visualization of the specific translation of the
signal in gonadotrophs.";
RL Endocrinology 139:5215-5223(1998).
RN [3]
RP SEQUENCE OF 147-302 FROM N.A., ALTERNATIVE SPLICING, AND TISSUE
SPECIFICITY.
RC TISSUE=Corpus luteum, and Fetal liver;
RA Anthony R.V., Smith G.W., Duong A., Pratt S.L., Smith M.F.;
RT "Two forms of the prolactin receptor messenger ribonucleic acid are
present in ovine fetal liver and adult ovary.";
RL Endocrine 3:291-295(1995).
CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone
prolactin.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 3 isoforms; 1/long/L-OPR (shown here),

```

2/short/S-OPR and 3/soluble; are produced by alternative splicing.
-!- TISSUE SPECIFICITY: Expressed in all tissues examined; liver,
pituitary, adrenal gland, ovary and fetal liver.
-!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
-!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

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EMBL; AF041257; AAB96795.1; -
EMBL; AF041977; AAB96920.1; -
EMBL; AF041979; AAB97082.1; -
EMBL; AF042358; AAB97744.1; -
EMBL; AF042358; AAB97744.1; -
EMBL; AF042358; AAB97743.1; -
EMBL; AF041978; AAB96965.1; -
EMBL; Y10578; CAA71597.1; -
EMBL; Y10808; CAA71766.1; -
HSP; P14787; IAN3.
InterPro: IPR002996; CRLA
InterPro: IPR003961; FN_III.
InterPro: IPR003528; Hemtopoptn_L_Fl.
Pfam: PF00041; fn3; 2.
SMART: SM00060; FN3; 2.
PROSITE; PS01352; HEMATOPOEC_L_Fl; 1.
Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
Alternative splicing 24
FT SIGNAL 1 POTENTIAL.
FT CHAIN 25 581 PROLACTIN RECEPTOR.
FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 238 258 POTENTIAL.
FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.
FT DOMAIN 123 227 FIBRONECTIN TYPE-III 2.
FT DISULFID 36 46 BY SIMILARITY.
FT DISULFID 75 86 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 132 132 GOSPEKPKLIKSPGKFTFCWEPFGADGGFLTNVTL
FT VARSPLIC 24 66 YRK -> ASDIYGGKSSVCTMYAFVGGIFLHMYLCV
FT VARSPLIC 67 581 DOYLLTVTS (IN ISOFORM 3).
FT VARSPLIC 286 296 MISSING (IN ISOFORM 3).
FT VARSPLIC 297 581 MISSING (IN ISOFORM 2).
FT VARSPLIC 281 281 I -> V (IN REF. 1; AAB97743/AAB97744).
FT CONFLICT 387 387 E -> K (IN REF. 2).
SQ SEQUENCE 581 AA; 65235 MW; EC534FDE538837A0 CRC64;

Query Match 9.2%; Score 209.5; DB 1; Length 581;
Best Local Similarity 26.8%; Pred. No. 2.2e-07;
Matches 61; Conservative 36; Mismatches 94; Indels 37; Gaps 10;

QY 112 PPARP-VVSCQAADYENFSCVTSQISGLPTRYLTSYRKTKVLGADSQRRSPSTGWPC 170
|| : : : : : || : : : : : || : : : : : || : : : : : || : : : : :
Db 27 PPEKPKLIKSPGKFTFCWEPFGADGGFLTNVTLTYRKE-----GETLIHEC 75

QY 171 PQPLGAGRCVVGAEF---WSQYRINVTENVPLG-ASTRLLDVSLQSLRPPDGLRV 226
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 76 PDYKGTGPNCSYFSKYTSIKWMYVITVSAINOMGISSDPLVDVTVIVEPEPPVNLTL 135

QY 227 ESYVPGYPRR--LRASNTYP-----ASWPCQPHFLKFLRYRPAQHPAWT--VEPAGLE 277
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 136 ELKHPEDRKPYLWIKWSPPTLTDVKGW-----FSIQYIRLKPKEATMETHFAPKLQ 190

QY 278 EVITDVAQLPHAVRSARDFLDAGTWSWSPAWGTPTGTIPKEIP 325
| : : : : : | : : : : : | : : : : : | : : : : : | : : : : :
Db 191 LKIFNLPGQKYLQIRCKP--DHGYWSEWSPE-----SFIQIPNDPF 231

RESULT 12
PRLR_BOVIN
ID PRLR_BOVIN STANDARD; PRT; 581 AA.
AC 028172; 018880; 046591.
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A. (LONG ISOFORM).
RC TISSUE=Endometrium;
RX MEDLINE=93246019; PubMed=1338725;
RA Scott P., Kessler M.A., Schuler L.A.;
RT "Molecular cloning of the bovine prolactin receptor and distribution
of prolactin and growth hormone receptor transcripts in fetal and
placental tissues.";
RT Mol. Cell. Endocrinol. 89:47-58(1992).
RN [2]
RP SEQUENCE FROM N.A. (SHORT ISOFORM), AND TISSUE SPECIFICITY.
RC TISSUE=Endometrium;
RX MEDLINE=97375450; PubMed=9231767;
RA Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;
RT "Prolactin receptor heterogeneity in bovine fetal and maternal
tissues.";
RT Mol. Cell. Endocrinol. 138:3187-3194(1997).
RN [3]
RP SEQUENCE OF 25-234 FROM N.A., AND SEQUENCE OF 25-33.
RC TISSUE=Mammary gland;
RX MEDLINE=95256770; PubMed=7738463;
RA Tchelet A., Statten N.R., Creely D.P., Krivi G.G., Gertler A.;
RT "Extracellular domain of prolactin receptor from bovine mammary gland:
its interaction with lactogenic hormones.";
RT J. Endocrinol. 144:393-403(1995).
RN [4]
RP ALTERNATIVE SPLICING.
RX MEDLINE=98001468; PubMed=9343303;
RA Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;
RT "Long and short forms of the ovine prolactin receptor: cDNA cloning
and genomic analysis reveal that the two forms arise by different
alternative splicing mechanisms in ruminants and in rodents.";
RT J. Mol. Endocrinol. 19:109-120(1997).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here)
and a short form; are produced by alternative splicing.
CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined; liver,
peripheral blood lymphocytes, endometrium, corpus luteum,
intestine, fetal thymus, fetal spleen, fetal liver and fetal
brain.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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EMBL; L02549; AAA51417.1; -
EMBL; AF027403; AAB83999.1; -
EMBL; AF042780; AAB97748.1; -
EMBL; AF042780; AAB97747.1; ALT_SEQ.

```
DR HSP; P14787; IAN3.
DR InterPro; IPR002996; CRIA.
DR InterPro; IPR003961; FN.III.
DR InterPro; IPR003528; Hemtopoptn_L_F1.
DR Pfam; PF00041; fn3; 2.
DR SMART; SM00060; FN3; 2.
DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;
KW Alternative splicing.
FT SIGNAL 1 24
FT CHAIN 25 581
FT DOMAIN 25 237
FT TRANSMEM 238 258
FT DOMAIN 259 581
FT DOMAIN 25 122
FT DOMAIN 123 227
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 132 132
FT VARSPIC 286
FT VARSPIC 297 581
FT CONFLICT 120 120
FT CONFLICT 128 128
FT CONFLICT 137 137
FT CONFLICT 141 141
FT CONFLICT 156 157
FT CONFLICT 186 186
FT SEQUENCE 581 AA; 65153 MW; 73850C0D6956E139 CRC64;

Query Match
Best Local Similarity 9.0%; Score 204.5; DB 1; Length 581;
Matches 61; Conservative 36; Mismatches 92; Indels 41; Gaps 11;

QY 112 PPARP-VVSCQAADYENFSCWSPQISGLPTRYLTYSYRKTVLGDADSGRRSPSTGPWPC 170
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 27 PPEKPKLVKCRSPGKETFTCWEPGADGGLPTNYLTTHKE-----GETLHEC 75

QY 171 PQDPLGAARCVVHG---AEFWQYRINVTENVPLG-ASTRLDVSLSQILRDPDPOGLRV 226
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 PDYKGGPNCSYFSKHTSIWVITVNAINOMGISSDPLVHVHYIVEPEPPANLTL 135

QY 227 ESVGYPYPR--LRASWTYP-----ASWPCQPHFLKFRLOYRPAQHPAWS---TVEPAG 275
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 136 ELKHEDRPKPYLWIKWSPPTMDVRSGW-----FIIQYEIRLKPEKATWETHFLKQIQ 190

QY 276 LEEVITDAVAGLPHAVRVRSARDFLDAGTWSTWSPGAMGTPSTGTIPKEIP 325
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 191 LK--IFNLYPGQKYLVOIRCKP--DHGYWSEWSPE-----SSIQIPNDFF 231
```

```
RESULT 13
PRLR_RABIT
ID PRLR_RABIT STANDARD; PRT; 616 AA.
AC P14787;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Prolactin receptor precursor (PRL-R).
GN PRLR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_Taxid=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Mammary gland;
RX MEDLINE=89184578; PubMed=2928371;
RA Edery M., Jolicoeur C., Levi-Meyrueis C., Dusanter-Fourt I.,
RA Petridou B., Boutin J.M., Lesueur L., Kelly P.A., Djiane J.;
RT "Identification and sequence analysis of a second form of prolactin
RT receptor by molecular cloning of complementary DNA from rabbit
```

```
RT mammary gland.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).
RN [2]
RP 3D-STRUCTURE MODELING OF 30-228.
RX MEDLINE=97248733; PubMed=9094747;
RA Halaby D., Thoreau E., Djiane J., Mornon J.-P.;
RT "Homology modeling of rabbit prolactin hormone complexed with its
RT receptor.";
RL Proteins 27:459-468(1997).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC
CC EMBL; J04510; AAA31457.1; -.
CC PIR; A30304; A30304.
CC PDB; IAN3; 03-DEC-97.
CC InterPro; IPR002996; CRIA.
CC InterPro; IPR003961; FN.III.
CC InterPro; IPR003528; Hemtopoptn_L_F1.
CC Pfam; PF00041; fn3; 2.
CC SMART; SM00060; FN3; 2.
CC PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.
KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat; 3D-structure.
FT SIGNAL 1 24
FT CHAIN 25 616
FT DOMAIN 25 234
FT TRANSMEM 235 258
FT DOMAIN 259 616
FT DOMAIN 25 122
FT DOMAIN 124 227
FT DISULFID 36 46
FT DISULFID 75 86
FT CARBOHYD 59 59
FT CARBOHYD 104 104
FT CARBOHYD 132 132
FT SEQUENCE 616 AA; 68840 MW; 80E3166FEF7108C CRC64;

Query Match
Best Local Similarity 9.0%; Score 204; DB 1; Length 616;
Matches 66; Conservative 29; Mismatches 95; Indels 48; Gaps 13;

QY 112 PPARP-VVSCQAADYENFSCWSPQISGLPTRYLTYSYRKTVLGDADSGRRSPSTGPWPC 170
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 27 PPEKPKLVKCRSPGKETFTCWMPGADGGLPTNYLTTHKE-----GETLHEC 75

QY 171 PQDPLGAARCVVHG---AEFWQYRINVTENVPLGAST---RLDVSLSQILRDPDPOGL 224
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 76 PDYKGGPNCSYFSKHTSIWVITVNAINOMGSSVSDPRVDVTV--IVEPDPVNL 133

QY 225 RVESVPGYPR--LRASWTYP-----ASWPCQPHFLKFRLOYRPAQHPAWSVTEPAGL 276
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 134 TLEVKHPEDRKPYLWVKWLPPTLVDRSGW-----LTLOYEIRLKPEKAAEWET-HFAQ 187

QY 277 EE--VITDAVAGLPHAVRVRSARDFLDAGTWSTWSPGAMGTPSTGTIP-----KEIPAW 327
|| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 188 QTQFKILSLYPGQKYLVOIRCKP--DHGFWSEWSPE-----SSIQIPNDFTMKDITW 238

RESULT 14
PRLR_CEREL
ID PRLR_CEREL STANDARD; PRT; 581 AA.
AC Q28235;
DT 01-NOV-1997 (Rel. 35, Created)
```



```
Db 65 SSEVL-----GSGKTLTILVKEFEDAGHYTCRR-----GGEVLSQMLLLHKNEDGIWST 114
QY 110 -----GYPPARPVWSCOAADYE-NFSCWTSPSQISGLPTRYLTSYKKTIVLGADSORRSP 163
Db 115 DILKKKEPENKNLVTCESAKNYSGRFTCMW-----LTAISTDVNFVSKSHRGSS 162
QY 164 STGPMWPCQDPLGAARCVVHGAEFWSQYRINVTEVNPGLGASTRLLDVS----- 211
Db 163 DPQGVTCGEATLSAERVKIEQREY-KKYSVQCEQEDNACPTAEETLPITVVVDVAVHKLKYE 221
QY 212 -----LQSILRPDPQGLRVESVPGYPRRLRASWTYPASWPCOPH--FLKFRLOQYRP 262
Db 222 NYISSFFIRDIIPDPKPKMKP-SKTPQQVEVTWEYKPDW-STPHSYFSLTFSVQVQG 279
QY 263 AOHPAWSTVEPAGLEVITDAVAGLPHAVRVARSARDFLDAGTWSTWS 308
Db 280 KKKKRSNTLH---VDKTSVTVCQKGVSVQVQARDRYNSWSWEA 322
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Search completed: January 17, 2003, 19:38:22
Job time : 18 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:37:20 ; Search time 22 Seconds
(without alignments)
1844.033 Million cell updates/sec

Title: US-09-924-338-2
Perfect score: 2275
Sequence: 1 MSSSCSGLSRVLVAVATALV.....KPGFLASVIPVDRPGAPNL 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2275	100.0	422	2	I37891
2	1897	83.4	432	2	I48343
3	395.5	17.4	460	2	JL0145
4	392	17.2	372	2	I38141
5	389.5	17.1	440	2	JL0144
6	380	16.7	362	2	S60614
7	379	16.7	372	1	UHHUCN
8	360	15.8	468	1	A41242
9	298.5	13.1	462	1	A37986
10	221	9.7	830	2	I50455
11	214	9.4	831	2	J01655
12	204.5	9.0	581	2	I45971
13	204	9.0	616	2	A30304
14	189	8.3	288	2	B59405
15	189	8.3	376	2	A59405
16	189	8.3	622	2	A40144
17	186	8.2	1265	1	A37967
18	183	8.0	310	2	A29884
19	183	8.0	412	2	A41070
20	183	8.0	610	2	A34631
21	183	8.0	610	2	A36116
22	174	7.6	292	2	I77525
23	174	7.6	303	2	I77524
24	174	7.6	608	2	I53269
25	173.5	7.6	630	2	I51086
26	167.5	7.4	328	2	I38957
27	166.5	7.3	761	1	IJHUNG
28	150	6.6	918	2	A36337
29	149.5	6.6	853	1	IJBONC

30	148	6.5	335	2	I72789	interleukin 12 p40
31	146.5	6.4	858	1	IJRTNC	neural cell adhesi
32	145	6.4	771	2	B38252	granulocyte colony
33	145	6.4	783	2	JH0329	granulocyte colony
34	145	6.4	863	2	C38252	granulocyte colony
35	143	6.3	1209	2	T42718	probable neural ce
36	142.5	6.3	1897	1	TDHULK	leukocyte antigen-
37	142	6.2	150	2	B34631	lactogen receptor
38	140.5	6.2	917	2	I49699	glycoprotein I30 -
39	140.5	6.2	1898	2	S46216	leukocyte antigen-
40	139.5	6.1	1092	2	JX0312	differentiation-st
41	138.5	6.1	805	2	S68441	leptin receptor, s
42	138.5	6.1	892	2	S68439	leptin receptor, s
43	138.5	6.1	894	2	S68437	leptin receptor, s
44	138.5	6.1	900	2	S68440	leptin receptor, s
45	138.5	6.1	1162	2	S68438	leptin receptor, s

ALIGNMENTS

RESULT 1

I37891
interleukin-11 receptor alpha chain - human
C:Species: Homo sapiens (man)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 03-Dec-1999
C:Accession: I37891; G01970; G01971
R:Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Minviell
Blood 86, 2534-2540, 1995
A:Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic
A:Reference number: I37891; MUID:95399754; PMID:7670098
A:Accession: I37891
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-422 <RES>
A:Cross-references: EMBL:Z38102; NID:g995653; PIDN:CAA86224.1; PID:g995654
R:Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A:Reference number: G08959
A:Accession: G01970
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-422 <VAN>
A:Cross-references: EMBL:U32323; NID:g975334; PIDN:AAB36491.1; PID:g975335
R:Van Leuven, F.
submitted to the EMBL Data Library, July 1995
A:Reference number: G08961
A:Accession: G01971
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-422 <VA2>
A:Cross-references: EMBL:U32324; NID:g975336; PIDN:AAB36492.1; PID:g975337
C:Genetics:
A:Introns: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 390/2; 418/1
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
F:120-310/Domain: cytokine receptor homology <CR>

Query Match	100.0%;	Score	2275;	DB 2;	Length	422;	
Best Local Similarity	100.0%;	Pred. No.	1.6e-143;				
Matches	422;	Conservative	0;	Mismatches	0;	Gaps	0;
QY	1	MSSSCSGLSRVLVAVATALV	ASASSPCQAWGPGVQYQOPGRSVKLCPCGVTAGDPVSWF	60			
Db	1	MSSSCSGLSRVLVAVATALV	ASASSPCQAWGPGVQYQOPGRSVKLCPCGVTAGDPVSWF	60			
QY	61	RDEPKLLQPGDGLGHELVLAQAADSTDEGTYICQTLDDGALGGTVTTLQGLYPPARPVWSC	120				
Db	61	RDEPKLLQPGDGLGHELVLAQAADSTDEGTYICQTLDDGALGGTVTTLQGLYPPARPVWSC	120				
QY	121	QAADYENFSCWSPSQISGLPTRYLTYSYRKKTVLGADSORRSPSTGWPCCQDPLGAARC	180				
Db	121	QAADYENFSCWSPSQISGLPTRYLTYSYRKKTVLGADSORRSPSTGWPCCQDPLGAARC	180				

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QY 181 VVHGAEFWSQYRINVTENVPLGASTRLLDVSLQSLRDPDPOGLRVESVPGYPRRLRASW 240
Db 181 VVHGAEFWSQYRINVTENVPLGASTRLLDVSLQSLRDPDPOGLRVESVPGYPRRLRASW 240
QY 241 TYPASWPCQPFLKFRLOYRPAQHPAWSTVEPAGLEEVITDVAAGLPHAVRVVSARDFLD 300
Db 241 TYPASWPCQPFLKFRLOYRPAQHPAWSTVEPAGLEEVITDVAAGLPHAVRVVSARDFLD 300
QY 301 AGTSTWSPAWGTPSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLOPHRLDHR 360
Db 301 AGTSTWSPAWGTPSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLOPHRLDHR 360
QY 361 DSVEQAVLASLGILSFLGLVAGALALGLWLRLRRGKDGSPKPGFASVIVPDRRPGAP 420
Db 361 DSVEQAVLASLGILSFLGLVAGALALGLWLRLRRGKDGSPKPGFASVIVPDRRPGAP 420
QY 421 NL 422
Db 421 NL 422

RESULT 2
I48343
N:Interleukin-11 receptor alpha-chain precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 31-Jan-2000
C:Accession: I48343; S51619
R:Neuhaus, H.; Bettenhausen, B.; Bilinski, P.; Simon-Chazottes, D.; Guenet, J.L.; Gossle
Dev. Biol. 166, 521-542, 1994
A:Title: et12, a novel putative type-1 cytokine receptor expressed during mouse embryoge
A:Reference number: I48343
A:Accession: I48343
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-432 <RES>
A:Cross-references: EMBL:X74953; NID:g673437; PIDN:CAA52908.1; PID:g673438
R:Hilton, D.J.; Hilton, A.A.; Raicevic, A.; Rakar, S.; Harrison-Smith, M.; Gough, N.M.;
EMBO J. 13, 4765-4775, 1994
A:Title: Cloning of a murine IL-11 receptor alpha-chain; requirement for gp130 for high
A:Reference number: S51619; MUID:95045367; PMID:7957045
A:Accession: S51619
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-432 <HIL>
A:Cross-references: EMBL:U14412; NID:g576454; PIDN:AAA53248.1; PID:g576455
C:Genetics:
A:Gene: Et12/IL11
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog
F:120-310/Domain: cytokine receptor homology <CRS>

Query Match 83.4%; Score 1897; DB 2; Length 432;
Best Local Similarity 83.5%; Pred. No. 1.8e-118;
Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1;

QY 1 MSSSCGSLRVLAVATALVSASSPCPAWGPVQYQGPGRSVKLCPCPGVTAGDPVSWF 60
Db 1 MSSSCGSLRVLAVATALVSASSPCPAWGPVQYQGPGRSVKLCPCPGVTAGDPVSWF 60
QY 61 RDGEPKLLQGDPSGLGHELVLAQADSTDEGYICOTLDGALGGTTLQOLGYPPARPVSC 120
Db 61 RDGSRLLQGDPSGLGHELVLAQVDSDEGYVCOTLDGVSQGMVTLKLGPPARPEVSC 120
QY 121 QAADYENFSCWSPQISGLPTRYLTYSRKKTVLGDASQRRSPSTGPWPCPDPLGAARC 180
Db 121 QAADYENFSCWSPQISGLPTRYLTYSRKKTVLGDASQRRSPSTGPWPCPDPLGAARC 180
QY 181 VVHGAEFWSQYRINVTENVPLGASTRLLDVSLQSLRDPDPOGLRVESVPGYPRRLRASW 240
Db 181 VVHGAEFWSQYRINVTENVPLGASTRLLDVSLQSLRDPDPOGLRVESVPGYPRRLRASW 240
QY 241 TYPASWPCQPFLKFRLOYRPAQHPAWSTVEPAGLEEVITDVAAGLPHAVRVVSARDFLD 300
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Db 241 TYPASWPCQPFLKFRLOYRPAQHPAWSTVEPAGLEEVITDVAAGLPHAVRVVSARDFLD 300
QY 301 AGTSTWSPAWGTPSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLOPHRLDHR 360
Db 301 AGTSTWSPAWGTPSTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLOPHRLDHR 360
QY 359 HRDSVEQAVLASLGILSFLGLVAGALALGLWLRLRRGKDGSPKPGFASVIVPDRRPG 418
Db 361 HRDPLEQAVLASLGILSFLGLVAGALALGLWLRLRRGKDGSPKPGFASVIVPDRRPG 420
QY 419 APNL 422
Db 421 IPNL 424

RESULT 3
JL0145
N:Interleukin-6 receptor precursor (clone lambda 301) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jan-2000
C:Accession: JL0145; S14543
R: Sugita, T.; Totsuka, T.; Saito, M.; Yamasaki, K.; Taga, T.; Hirano, T.; Kishimoto,
J. Exp. Med. 171, 2001-2009, 1990
A:Title: Functional murine interleukin 6 receptor with the intracisternal a particle
A:Reference number: JL0144; MUID:90278354; PMID:2112585
A:Accession: JL0145
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-460 <SUG>
A:Cross-references: GB:X51975; NID:g49725; PIDN:CAA36237.1; PID:g49726
A:Experimental source: clone lambda 301
R: Florillo, M.T.; Ciliberto, G.; Dente, L.
submitted to the EMBL Data Library, July 1990
A:Description: Cloning and expression of murine IL-6 receptor.
A:Reference number: S14543
A:Accession: S14543
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-373, 'R', 375-460 <FIO>
A:Cross-references: EMBL:X53802; NID:g52692; PIDN:CAA37810.1; PID:g52693
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immu
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-460/Product: interleukin-6 receptor #status predicted <MAT>
F:40-94/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:358-385/Domain: transmembrane #status predicted <TRA>

Query Match 17.4%; Score 395.5; DB 2; Length 460;
Best Local Similarity 30.7%; Pred. No. 5.8e-19;
Matches 145; Conservative 58; Mismatches 178; Indels 91; Gaps 25;

QY 1 MSSSCGSLRVLAVATALVSASSPCPAWGPVQYQGPGRSVKLCPCPGVTAGDPVSWF 58
Db 2 LTVGCTLLVALLAPAVALVLGS--CRALEVANGTIVTSLPGATVTLICPGKEAAGNVTH 59
QY 59 WFRDGEPEKLLQGDPSGLGHELVLAQADSTDEGYICOTLDGALGGTTLQOLGYPPARPV 117
Db 60 WYVSGS-----QNRWTTTGNLVLRLVDQLSDTDGYLC--SLNDHLVGTVPVLLVDVPPPEPK 114
QY 118 VSC-QAADYENFSCWSPQISGLPTRYLTYSRKKTVLGDASQRRSPSTGPWPCPDPL 175
Db 115 LSCFRKNPLVNAICEWRPSSTPS-PTTKAVLFAKKI-----NTTNGKSDFOVPCQYSQOL 168
QY 176 GAARCVVHGAEFWSQYRI-NVTEVNPILGASTRLLDV--SLQSLRDPDPOGLRVESVPGY 232
Db 169 KSFSCQVEILEGDKVYHIVSLCVANSVSSKSHNEAFHSLK-MVQDPDPANLVVSAIPGR 227
QY 233 PRRLRASWTYPASWPCQPFLKFRLOYRPAQHPAWSTVEPAGLEEVITDVAAG 286
Db 228 PRWLKVSQHPETWD-PSYLLQQLRAYR---PWSKEFTVLLLPVAYQYOCVITHDALRG 282
```


C;Comment: This growth factor receptor does not have a tyrosine kinase domain.

C:Genetics:
A:Gene: GDB: IL6R
A:Cross-references: GDB:l127966; OMIM:l147880
A:Map position: lq21-lq21
C:Superfamily: ciliary neurotrophic factor receptor; cytokine receptor; glycoprotein; immunoglobulin heavy chain variable domain
C:Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein
F:l-19/Domain: signal sequence #status predicted <SIG>
F:20-468/Product: interleukin-6 receptor #status predicted <MAT>
F:20-363/Domain: extracellular #status predicted <EXT>
F:40-98/Domain: immunoglobulin homology <IMM2>
F:l21-309/Domain: cytokine receptor homology <CRS>
F:364-386/Domain: transmembrane #status predicted <TM>
F:387-468/Domain: intracellular #status predicted <INT>
F:47-96/Dissulfide bonds: #status predicted
F:55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match	15.8%	Score 360;	DB 1;	Length 468;
Best Local Similarity	28.4%;	Pred. No. 1.3e-16;		
Matches 129;	Conservative	57;	Mismatches 196;	Indels 72;
				Gaps 19;

Qy	1	MSSCSGLSRVLVAVATALVSASSPCQAWPPGVGYOGGRSVKLCPCGVTAGD--PVS	58
Db	2	LAVGCALLAALLAAPGAAL--APRCPAQOEVARGLVSLPGDSVTLTCGVEPEDNATVH	59
Qy	59	WFRDGEPKLLGGPD-----SGLGHELVLAQADSTDECTYICQFLDCAIGCTVYLQIG	110
Db	60	W-----VLRKFAAGSHPSRWAGMGRLLRSLVSQJHDSGNVSCYRA-GRPAGTVHLLVD	111
Qy	111	YPPARPVVC--QAADYENFSGTWSQISGLPTRYLTSYRKKTIVLGADSQRSPTSG-PW	168
Db	112	VPDEPQLSCFRKSPISNVVCEMGPRSTVSLTT-----KAVLVRVFOINSAPDEFOE	163
Qy	169	PC-----PQDPLGAARCVVHGAEFWSQYRINVTENVPLGAS-TRLLDVLSQSLRPDPPOG	223
Db	164	PCQYSQESQKFSQOLAVPEGDS--SFVIVSMCVASSVSGSKFSKTQTFQCGGILQDPDPAN	221
Qy	224	LRVESVPGYPRRLRASWTYPASWPCOPHLLKFLQYRPAQHPAWSTVEPAGLEE--VIT	281
Db	222	ITVTAVARNPRWLVSVTWQDPHSWN--SSFYRLRFLRYRAERSKTFFTVMVKDQLQHCVJH	280
Qy	282	DAVAGLPFAHVRVSARQFLDAGTWTSPSAWGPSTGTITKEIPAMGQLHTOPEVSPQD	341
Db	281	DANSGLRHVQLRAQEEFGQGESEWSPEAMGTPWTES-----RSPPAENEVS	328
Qy	342	SPAPPRPSLQHPRLLRDRSVSEQAV---LASGLILSFLGLVAGALAG-----	388
Db	329	TPMOALTNNKDDNLI--FRDSANATSLPYODSSSVLPPTFL-VAGSFAFGTLLGIAVL	386

```

RESULT 9
A37986
interleukin-6 receptor precursor - rat
N;Alternate names: IL-6 receptor
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Jun-1993 #sequence_revision
C;Accession: A37986
#text_change 22-Jun-1999

```

J. Biol. Chem. 265, 19853-19862, 1990
A;Title: Molecular cloning, characterization and functional expression of the rat liver A;
Reference number: A37986; MUID:91060602; PMID:2174054

A; Molecule type: mRNA
A; Residues: 1-462 <BAU>
A; Cross-references: GB:M59587; GB:J05668; NID:G204921; PID:AAA41431.1; PID:G204922
C; Comment: After binding IL-6, this chain associates with a 130K glycoprotein that
C; Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; imu
C; Keywords: acute phase; cytokine receptor; transmembrane protein
F; 1-19/Domain: signal sequence #start predicted <SIG>

F:20-462/Product: interleukin-6, receptor #status predicted <MAT>
F:20-364/Domain: extracellular #status predicted <EXT>
F:40-96/Domain: immunoglobulin homology <IMM>
F:117-306/Domain: cytokine receptor homology <CRS>
F:363-385/Domain: transmembrane #status predicted <TM>
F:386-462/Domain: intracellular #status predicted <INT>
F:47-92/Disulfide bonds: #status predicted

Query Match	13.1%	Score 298.5;	DB 1;	Length 462;
Best Local Similarity	27.2%	Pred. No. 1.6e-12;		
Matches 132; Conservative	50;	Mismatches 181;	Indels 123;	Gaps 25;

[illegible]

RESULT 10
I50455

prolactin receptor - pigeon
C/Species: Columba livia (domestic pigeon)
C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000
C/Accession: I50455
R/Chen, X.; Horseman, N.D.
Endocrinology 135, 269-276, 1994
A/Title: Cloning, expression, and mutational analysis of the pigeon prolactin
A/Reference number: I50455; MUID:94283267; PMID:7516866

A:Accession: J10433
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-830 <CHE>
 A:Cross-references: EMBL:U07694; NID:g466381; PID:
 C:Superfamily: cytokine receptor homology
 F:340-220/Domain: cytokine receptor homology <CRS1>
 F:340-426/Domain: cytokine receptor homology <CRS2>

Query Match 9.7%; Score 221; DB 2; Length 830;
Best Local Similarity 29.0%; -Pred. No. 4e-07;
Matches 67; Conservative 36; Mismatches 90; Indels

QV 111 YPPARPVVSCOAADYENFSCWTWSPSOISGLPTRYLTSYRKKTVLGADSORRSPSTGPWPC 170

Endocrinology 135, 269-276, 1994

Db 27 YGKPKIIRCSLEKETFSCWKKPGSDGLPTNYTLFYSK-----DSEKI-----YEC 75
QY 171 PODPL-GAARCVV--HGAEFWSQYRINTEVNPGLAST---RLLDVSLQSLIRPDPPOGL 224
Db 76 PDYMGSGNSCYFEDKXHNTPWYTYNITVYMAWNEIGNSSDPOYVDVT--SIVQPDAPVNL 133
QY 225 RVESVPGYPRRLRASWTY-PASWPCQP-----HFLKLFRLQYRPAQHPAWSTVEPAGL 276
Db 134 SLET-----KTSASTTYLLAKWSPPLADVTSNSHVYRLELRLKPEKEWEIVS-VGV 186
QY 277 EE--VITDAVAGLPHAVRVRSARDFLDAGTWSWPEANGTPTSTGTPKEIP 325
Db 187 QYQVKNRLOAGVYVQV--RCVLDIGSEWSSSERHIHPNGESPPEKP 235
RESULT 11
QY1655
prolactin receptor precursor - chicken
C:Species: Gallus gallus (chicken)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
C:Accession: JQ1655
R:Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
Biochem. Biophys. Res. Commun. 188, 490-496, 1992
A:Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA se
A:Reference number: JQ1655; MUID:93075121; PMID:1445292
A:Molecule type: mRNA
A:Residues: 1-831 <TAN>
A:Cross-references: DDBJ:D13154; NID:g222848; PIDN:BAA02439.1; PID:g222849
A:Experimental source: Kidney
C:Superfamily: cytokine receptor homology
C:Keywords: glycoprotein; transmembrane protein
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-831/Product: prolactin receptor #status predicted <MAT>
F:36-219/Domain: cytokine receptor homology <CRS1>
F:239-425/Domain: cytokine receptor homology <CRS2>
F:439-462/Domain: transmembrane #status predicted <TM>
F:59,91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (asn) (coval
Query Match 9.4%; Score 214; DB 2; Length 831;
Best Local Similarity 27.5%; Pred. No. 1.2e-06;
Matches 76; Conservative 42; Mismatches 108; Indels 50; Gaps 15;
QY 113 PARP-VVSCQAADYENFSCWSPSQISGLPTRYLTYSYRKKTVLGADSORSPSTGWPWCP 171
Db 28 PGKPKIIRCSLEKETFSCWKKPGSDGLPTNYTLFYSK-----DSEKI-----YEC 76
QY 172 Q-DPLGAARCVV--HGAEFWSQYRINTEVNPGLAST---RLLDVSLQSLIRPDPPOGLR 225
Db 77 DYRTSGPNSCYFNKNHTSPWNTNITVATNEIGNSSDPOYVDVT--SIVQPGSPVNL 134
QY 226 VESVPGYPRR-----LRASWTYPASWPCOPHLLKFLRQYRPAQHPAWSTVEPAGLEE- 278
Db 135 LET-----KRSANIMYLWAKWSPPLADASSNHLHYELRIKPEKEWETIS-VGVQ 188
QY 279 -VITDAVAGLPHAVRVRSARDFLDAGTWSWPEANGTPTSTGTPKEIPAWQLHTQPEVE 337
Db 189 CKINRLNAGRYVQV--RCTLDPGSEWSSSERHILIPSGOSPPEKPTTIKCRS-PERE 245
QY 338 -----POVDSAPPRLPSLOPHRLHSDSVEQ 366
Db 246 TETCWMKPGLDGGHTNYT-----LLYSKEGEQV 275
RESULT 12
I45971
prolactin receptor - bovine
C:Species: Bos primigenius taurus (cattle)
C:Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
C:Accession: I45971
R:Scott, P.; Kessler, M.A.; Schuler, L.A.
Mol. Cell. Endocrinol. 89, 47-58, 1992

A:Title: Molecular cloning of the bovine prolactin receptor and distribution of prola
A:Reference number: I45971; MUID:93246019; PMID:1338725
A:Accession: I45971
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 1-581 <SCO>
A:Cross-references: GB:I02549; NID:g163617; PIDN:AAA51417.1; PID:g163618
C:Genetics:
A:Gene: PRUR
C:Superfamily: cytokine receptor homology
F:36-221/Domain: cytokine receptor homology <CRS>
Query Match 9.0%; Score 204.5; DB 2; Length 581;
Best Local Similarity 26.5%; Pred. No. 3.4e-06;
Matches 61; Conservative 36; Mismatches 92; Indels 41; Gaps 11;
QY 112 PPARP-VVSCQAADYENFSCWSPSQISGLPTRYLTYSYRKKTVLGADSORSPSTGWPWCP 170
Db 27 PPEKPKLVKCRSPGKETFTCWEPGADGGLPTNYTLTYHKE-----GETLIHEC 75
QY 171 PQDPLGAARCVVHG---AEFWWSQYRINTEVNPGLG-ASTRLLDVSLQSLIRPDPPOGLRV 226
Db 76 PDYKTCGPNSCYFSKKTHTSIKMWIVITVNAINQMGISSDPLYVHVYIVVEPEPANLTL 135
QY 227 ESVPGYPRR--LRASWTYP-----ASWPCOPHLLKFLRQYRPAQHPAWS---TVEPAG 275
Db 136 ELKHPEDRKPYLWIKWSPPTMTDVKSGW-----PIIQVEIRLKEKATDWTHTLQQTQ 190
QY 276 LEEVITDAVAGLPHAVRVRSARDFLDAGTWSWPEANGTPTSTGTPKEIP 325
Db 191 LK--IFNLYPGQKYLVOIRCKP--DHGYWSEWSPE-----SSIQIPNDPF 231
RESULT 13
A30304
prolactin receptor 2 precursor - rabbit
N:Alternate names: prolactin receptor, mammary gland
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 28-Jul-2000
C:Accession: A30304; A60380
R:Edery, M.; Jolicoeur, C.; Levi-Meyrueis, C.; Dusanter-Fourt, I.; Petridou, B.; Bout
Proc. Natl. Acad. Sci. U.S.A. 86, 2112-2116, 1989
A:Title: Identification and sequence analysis of a second form of prolactin receptor
A:Reference number: A30304; MUID:89184578; PMID:2928321
A:Accession: A30304
A:Molecule type: mRNA
A:Residues: 1-616 <EDE>
A:Cross-references: GB:J04510; NID:g165669; PIDN:AAA31457.1; PID:g165670
R:Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
Int. J. Biochem. 22, 1089-1095, 1990
A:Title: Purification and partial sequence of the rabbit mammary gland prolactin rece
A:Reference number: A60380; MUID:91146782; PMID:2289615
A:Accession: A60380
A:Molecule type: protein
A:Residues: 41-58, 'X', 60-66; 90-93, 'X', 95-96, 'X', 98-103, 'X', 105, 'NX', 108, 150-164, 'XX',
A:Note: The amino end of the mature protein was blocked
C:Superfamily: cytokine receptor homology
C:Keywords: blocked amino end; glycoprotein; transmembrane protein
F:1-24/Domain: signal sequence #status predicted <SIG>
F:25-616/Product: prolactin receptor 2 #status predicted <MAT>
F:36-221/Domain: cytokine receptor homology <CRS>
F:235-258/Domain: transmembrane #status predicted <TM>
F:59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicte
Query Match 9.0%; Score 204; DB 2; Length 616;
Best Local Similarity 27.7%; Pred. No. 3.9e-06;
Matches 66; Conservative 29; Mismatches 95; Indels 48; Gaps 13;
QY 112 PPARP-VVSCQAADYENFSCWSPSQISGLPTRYLTYSYRKKTVLGADSORSPSTGWPWCP 170
Db 27 PPGKPFIFKCRSPGKETFTCWWRPGADGGLPTNYTLTYHKE-----GETITHEC 75
QY 171 PQDPLGAARCVVHG---AEFWWSQYRINTEVNPGLAST---RLLDVSLQSLIRPDPPOGL 224

Db 76 PDYKGTGPNSCYFSKKHTSIWTIIIVTNATNOMSSVSDPRYVDVTV--IVEPDPVNL 133
QY 225 RVESVPCYPRR--LRASWTYP-----ASWPCQPHLLKRLQYRPAQHAWSTVEAGL 276
Db 134 TLEVKHEDRKPYLWVKWLPPTLVDRVSGW-----LFLQYEIRLKPKEAAEWET-HEAGQ 187
QY 277 EE--VITDAVAGLPHAVRVVSARDFLDAGTWSPEAWGTPSTGTIP-----KEIPAW 327
Db 188 QTQPKILSLYPGQKYLQVRCRP--DHGFWSVMSPE-----SSIIQIENDTMRKDIYTW 238

RESULT 14

B59405

prolactin receptor short form Slb precursor, breast cancer cells T-47D - human

C:Species: Homo sapiens (man)

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Mar-2002

C:Accession: B59405; B49400

R:Hu, Z.Z.; Meng, J.; Dufau, M.L.

J. Biol. Chem. 276, 41086-41094, 2001

A:Title: Isolation and characterization of two novel forms of the human prolactin receptor

A:Reference number: A59405; MUID:21538812; PMID:11518703

A:Accession: B59405

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-288 <HU1>

A:Cross-references: GB:AF214012; PIDN:AF214012.1

R:Hu, Z.Z.

submitted to GenBank, December, 1999

A:Reference number: A49400

A:Accession: B49400

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-288 <HU2>

A:Cross-references: GB:AF214012; PIDN:AF214012.1

A:Comment: This is one of the short forms (Slb and Slb) of the human prolactin receptor

ta-casain gene promoter activation, with Slb more effective than Slb. However, their lig

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: 5p13.3-5p13.1

C:Superfamily: cytokine receptor homology

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-288/Product: prolactin receptor, short form Slb #status predicted <MAT>

F:36-221/Domain: cytokine receptor homology <CRS>

F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.3%; Score 189; DB 2; Length 288;

Best Local Similarity 28.2%; Pred. No. 1.7e-05;

Matches 60; Conservative 27; Mismatches 92; Indels 34; Gaps 10;

QY 112 PPARP-VVSCQADYENFSCSTWSPSQISGLPTRYLTYSYRKTKVLGADSQRRSPSTGPWPC 170

Db 27 PPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNYSLT-----HREGETLMHEC 75

QY 171 PQDPLGAARCVVHGAEEF---WSQYRINVTENVPLGAS--TRLLDVSLOSILRPPDPPQGLRV 226

Db 76 PDYITGPNNSCHFCGKQYTSMTWRTYIMVMVATNQMSSFSDELYVDVTYIVQDPDPLEAV 135

QY 227 ESVPGYPRR--LRASWTYP-----ASWPCQPHLLKRLQYRPAQHAWSTVEPAG--L 276

Db 136 EVKQPEDRKPYLWKWSPPPTLIDLKTGW-----FTLLYEIRLKPKEAAEWI-IHFAGQQT 189

QY 277 EEVITDAVAGLPHAVRVVSARDFLDAGTWSPEAWGTPSTGTIP-----KEIPAW 327

Db 190 EFKILSLHPGQKYLQVRCRP--DHGFWSVMSPE-----SSIIQIENDTMRKDIYTW 238

RESULT 15

A59405

prolactin receptor short form Slb precursor, breast cancer cells T-47D - human

C:Species: Homo sapiens

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Mar-2002
C:Accession: A59405; A49400
R:Hu, Z.Z.; Meng, J.; Dufau, M.L.
J. Biol. Chem. 276, 41086-41094, 2001
A:Title: Isolation and characterization of two novel forms of the human prolactin rec
A:Reference number: A59405; MUID:21538812; PMID:11518703
A:Accession: A59405
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-376 <HU1>
A:Cross-references: GB:AF214012; PIDN:AF214012.1
R:Hu, Z.Z.
submitted to GenBank, December, 1999

A:Reference number: A49400

A:Accession: A49400

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-376 <HU2>

A:Cross-references: GB:AF214012; PIDN:AF214012.1

A:Comment: This is one of the short forms (Slb and Slb) of the human prolactin recept

eta-casain gene promoter activation, with Slb less effective than Slb. However, their

ted COS-1 and HEK293 cells is due to rapid intracellular turnover of the receptor. #e

C:Genetics:

A:Gene: GDB:PRLR

A:Cross-references: GDB:120315; OMIM:176761

A:Map position: 5p13.3-5p13.1

C:Superfamily: cytokine receptor homology

C:Keywords: glycoprotein; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-376/Product: prolactin receptor, short form Slb #status predicted <MAT>

F:36-221/Domain: cytokine receptor homology <CRS>

F:59,104,233/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 8.3%; Score 189; DB 2; Length 376;

Best Local Similarity 28.2%; Pred. No. 2.2e-05;

Matches 60; Conservative 27; Mismatches 92; Indels 34; Gaps 10;

QY 112 PPARP-VVSCQADYENFSCSTWSPSQISGLPTRYLTYSYRKTKVLGADSQRRSPSTGPWPC 170

Db 27 PPGKPEIFKCRSPNKETFTCWWRPGTGGGLPTNYSLT-----HREGETLMHEC 75

QY 171 PQDPLGAARCVVHGAEEF---WSQYRINVTENVPLGAS--TRLLDVSLOSILRPPDPPQGLRV 226

Db 76 PDYITGPNNSCHFCGKQYTSMTWRTYIMVMVATNQMSSFSDELYVDVTYIVQDPDPLEAV 135

QY 227 ESVPGYPRR--LRASWTYP-----ASWPCQPHLLKRLQYRPAQHAWSTVEPAG--L 276

Db 136 EVKQPEDRKPYLWKWSPPPTLIDLKTGW-----FTLLYEIRLKPKEAAEWI-IHFAGQQT 189

QY 277 EEVITDAVAGLPHAVRVVSARDFLDAGTWSPEAWGTPSTGTIP-----KEIPAW 309

Db 190 EFKILSLHPGQKYLQVRCRP--DHGFWSVMSPE-----SSIIQIENDTMRKDIYTW 220

Search completed: January 17, 2003, 19:39:58

Job time : 26 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:38:14 ; Search time 13 Seconds
(without alignments)
645.287 Million cell updates/sec

Title: US-09-924-338-2

Perfect score: 2275

Sequence: 1 MSSSCSLGRVLVAVATALV.....KPGFLASVIPDRRPGAPNL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PublishedApplications_AA:

1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB pep.*
6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB pep.*
7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB pep.*
11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB pep.*
12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB pep.*
13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB pep.*
14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match %	Score	Length	DB ID	Description
1	2275	100.0	422	10	US-09-924-338-2
2	1831	80.5	441	10	US-09-924-338-4
3	339	14.9	1158	9	US-09-935-868-26
4	332	14.6	1168	9	US-09-935-868-24
5	329.5	14.5	360	9	US-09-935-868-15
6	329.5	14.5	592	9	US-09-935-868-8
7	315	13.8	315	9	US-09-935-868-16
8	255.5	11.2	229	9	US-10-000-776-10
9	255.5	11.2	229	9	US-09-791-497-12
10	212.5	9.3	389	10	US-09-880-578-27
11	211.5	9.3	389	10	US-09-880-578-24
12	211.5	9.3	389	10	US-09-880-578-29
13	211.5	9.3	421	10	US-09-037-657-44
14	211.5	9.3	422	9	US-09-944-413-32
15	211.5	9.3	422	9	US-09-944-403-32
16	211.5	9.3	422	9	US-09-944-896-32
17	211.5	9.3	422	9	US-09-944-944-32
18	211.5	9.3	422	9	US-09-944-907-32
19	211.5	9.3	422	9	US-09-944-929-32

20	211.5	9.3	422	10	US-09-866-028-32	Sequence 32, Appl
21	211.5	9.3	422	10	US-09-944-449-32	Sequence 32, Appl
22	211.5	9.3	422	10	US-09-944-457-32	Sequence 32, Appl
23	211.5	9.3	422	10	US-09-944-862-32	Sequence 32, Appl
24	211.5	9.3	422	10	US-09-945-587-32	Sequence 32, Appl
25	211.5	9.3	422	10	US-09-945-015-32	Sequence 32, Appl
26	211.5	9.3	422	10	US-09-944-396-32	Sequence 32, Appl
27	211.5	9.3	422	10	US-09-944-097-32	Sequence 32, Appl
28	211.5	9.3	422	10	US-09-944-432-32	Sequence 32, Appl
29	211.5	9.3	422	10	US-09-943-762-32	Sequence 32, Appl
30	211.5	9.3	422	10	US-09-944-654-32	Sequence 32, Appl
31	211.5	9.3	422	10	US-09-943-851A-32	Sequence 32, Appl
32	211.5	9.3	425	10	US-09-880-578-4	Sequence 4, Appl
33	210.5	9.3	389	10	US-09-880-578-22	Sequence 22, Appl
34	210.5	9.3	389	10	US-09-880-578-25	Sequence 25, Appl
35	210.5	9.3	389	10	US-09-880-578-26	Sequence 26, Appl
36	210.5	9.3	389	10	US-09-880-578-30	Sequence 30, Appl
37	210.5	9.3	392	10	US-09-880-578-18	Sequence 18, Appl
38	210.5	9.3	422	10	US-09-880-578-2	Sequence 2, Appl
39	209.5	9.2	389	10	US-09-880-578-28	Sequence 28, Appl
40	209.5	9.2	405	9	US-10-074-901-2	Sequence 2, Appl
41	209.5	9.2	413	10	US-09-037-657-13	Sequence 13, Appl
42	209.5	9.2	425	10	US-09-037-657-15	Sequence 15, Appl
43	207.5	9.1	303	10	US-09-880-578-23	Sequence 23, Appl
44	207.5	9.1	385	10	US-09-880-578-19	Sequence 19, Appl
45	207.5	9.1	385	10	US-09-880-578-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1
US-09-924-338-2
; Sequence 2, Application US/09924338
; Patent No. US20020082233A1
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLEUKIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/924,338
; FILING DATE: 07-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/151,102
; FILING DATE: 1998-09-10
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-924-338-2
Query Match      100.08; Score 2275; DB 10; Length 422;
Best Local Similarity 100.08; Pred. No. 5e-144;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MSSSCSGLSRVLAVATLVASSPCPAWPGVQYQPGRSVKLCCGCGVGTAGDPVSWF 60
Db 1 MSSSCSGLSRVLAVATLVASSPCPAWPGVQYQPGRSVKLCCGCGVGTAGDPVSWF 60
Oy 61 RDGEPKLLQGPDSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVYSC 120
Db 61 RDGEPKLLQGPDSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVYSC 120
Oy 121 QAADYENFSCWTSQISGLTRVLTYSRKKTIVLGADSORRSPSTGWPCCQDPPLGAARC 180
Db 121 QAADYENFSCWTSQISGLTRVLTYSRKKTIVLGADSORRSPSTGWPCCQDPPLGAARC 180
Oy 181 VVHGAEFWSQYRINVTENVPLGASTRLLDVLSQSLRLRDPPOGLRVESVPGYPRRLRASW 240
Db 181 VVHGAEFWSQYRINVTENVPLGASTRLLDVLSQSLRLRDPPOGLRVESVPGYPRRLRASW 240
Oy 241 TYPASWPCQPHFLKFRLOYPRAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFLD 300
Db 241 TYPASWPCQPHFLKFRLOYPRAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFLD 300
Oy 301 AGTWSTWPEAWGTPSTGTIPKEIPAWGQLHTQPEVQVDSPPAPRPSLQPHRLLDHR 360
Db 301 AGTWSTWPEAWGTPSTGTIPKEIPAWGQLHTQPEVQVDSPPAPRPSLQPHRLLDHR 360
Oy 361 DSVEQVAVLASIGLSFLGLVAGALALGLMLRRLRGKDGSPKPGFLASVTPVDRRPGAP 420
Db 361 DSVEQVAVLASIGLSFLGLVAGALALGLMLRRLRGKDGSPKPGFLASVTPVDRRPGAP 420
Oy 421 NL 422
Db 421 NL 422
RESULT 2
US-09-924-338-4
; Sequence 4, Application US/09924338
; Patent No. US20020082233A1
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/924,338
; FILING DATE: 07-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/151,102
; FILING DATE: 1998-09-10
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15252
;
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-924-338-2
Query Match      100.08; Score 2275; DB 10; Length 422;
Best Local Similarity 100.08; Pred. No. 5e-144;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MSSSCSGLSRVLAVATLVASSPCPAWPGVQYQPGRSVKLCCGCGVGTAGDPVSWF 60
Db 1 MSSSCSGLSRVLAVATLVASSPCPAWPGVQYQPGRSVKLCCGCGVGTAGDPVSWF 60
Oy 61 RDGEPKLLQGPDSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVYSC 120
Db 61 RDGEPKLLQGPDSGLGHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVYSC 120
Oy 121 QAADYENFSCWTSQISGLTRVLTYSRKKTIVLGADSORRSPSTGWPCCQDPPLGAARC 180
Db 121 QAADYENFSCWTSQISGLTRVLTYSRKKTIVLGADSORRSPSTGWPCCQDPPLGAARC 180
Oy 181 VVHGAEFWSQYRINVTENVPLGASTRLLDVLSQSLRLRDPPOGLRVESVPGYPRRLRASW 240
Db 181 VVHGAEFWSQYRINVTENVPLGASTRLLDVLSQSLRLRDPPOGLRVESVPGYPRRLRASW 240
Oy 241 TYPASWPCQPHFLKFRLOYPRAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFLD 300
Db 241 TYPASWPCQPHFLKFRLOYPRAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFLD 300
Oy 301 AGTWSTWPEAWGTPSTGTIPKEIPAWGQLHTQPEVQVDSPPAPRPSLQPHRLLDHR 360
Db 301 AGTWSTWPEAWGTPSTGTIPKEIPAWGQLHTQPEVQVDSPPAPRPSLQPHRLLDHR 360
Oy 361 DSVEQVAVLASIGLSFLGLVAGALALGLMLRRLRGKDGSPKPGFLASVTPVDRRPGAP 420
Db 361 DSVEQVAVLASIGLSFLGLVAGALALGLMLRRLRGKDGSPKPGFLASVTPVDRRPGAP 420
Oy 421 NL 422
Db 421 NL 422
RESULT 2
US-09-924-338-4
; Sequence 4, Application US/09924338
; Patent No. US20020082233A1
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/924,338
; FILING DATE: 07-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/151,102
; FILING DATE: 1998-09-10
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15252
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 441 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-924-338-4
Query Match      80.5%; Score 1831; DB 10; Length 441;
Best Local Similarity 83.1%; Pred. No. 1.5e-114;
Matches 340; Conservative 17; Mismatches 50; Indels 2; Gaps 1;
Oy 16 ATALVSASSPCPAWPGVQYQPGRSVKLCCGCGVGTAGDPVSWFRDGEKLLQGPDSGL 75
Db 25 ATALVSASSPCPAWPGVQYQPGRPVLMCCPCGSAGTPEVFRDGDRLQGPDSGL 84
Oy 76 GHELVLAQADSTDEGTYICQTLDGALGGTTLQLGYPARPVWSCQAADYENFSCWTSPS 135
Db 85 GHELVLAQVDSDEGTYVQCQTLDCVSGMWTLKLGFPARPPEVSCQAVDYENFSCWSPG 144
Oy 136 QISGLPTRYLTYSRKKTIVLGADSORRSPSTGWPCCQDPPLGAARCVVHGAEFWSQYRIN 195
Db 145 QVSGLPTRYLTYSRKKTLPGAESQRESPTGWPCCQDPPLGAARCVVHGAEFWSQYRIN 204
Oy 196 TEVNPGLASTRLLDVLSQSLRLRDPPOGLRVESVPGYPRRLRASWTYPASWPCQPHFLK 255
Db 205 TEVNPGLASTRLLDVLSQSLRLRDPPOGLRVESVPGYPRRLHASWTYPASWRRQPHFLK 264
Oy 256 FRLOYPRAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFLDAGTWSTWSPGAWGTP 315
Db 265 FRLOYPRAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFLDAGTWSTWSPGAWGTP 324
Oy 316 STGTIPKEIPAWGQLHTQ--PEVEPQVDSPPAPRPSLQPHRLLDHRDSVEQVAVLASLG 373
Db 325 STGTIPKEIPAWGQLHTQ--PEVEPQVDSPPAPRPSLQPHRLLDHRDSVEQVAVLASLG 384
Oy 374 ILSFLGLVAGALALGLMLRRLRGKDGSPKPGFLASVTPVDRRPGAPNL 422
Db 385 ILSFLGLVAGALALGLMLRRLRGKDGSPKPGFLASVTPVDRRPGAPNL 433
RESULT 3
US-09-935-868-26
; Sequence 26, Application US/09935868
; Patent No. US2002016490A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 26
; LENGTH: 1158
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-26
Query Match      14.9%; Score 339; DB 9; Length 1158;
Best Local Similarity 30.4%; Pred. No. 4.1e-15;
Matches 112; Conservative 45; Mismatches 169; Indels 42; Gaps 14;
Oy 5 CSGLSRVLAVATLVASSPCPAWPGVQYQPGRSVKLCCGCGVGTAGD--PVSWFRD 62
Db 6 CALLAALLAAPGAAL--APRRCPAQAEVARGVLTSLPGDSVTLTCTCGVEPEDNATVHW--- 60
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Qy 63 GEPKLLQGPD-----SGLGHELVLAQADSTDEGTICQTLGALGGTTLQLGYPPA 114
Db 61 ----VLRKPAAGSHPSRWAGMGRLLRSVLHDSGNTSCYRA--GRPAGTVHLLVDVPE 115
Qy 115 RPVWSC-QAADYENFSCWSPSQISGLPTRYLTSYRKKTVLGADSORSPSTG--PWPC-- 170
Db 116 EPQLSCFRKSPLSNVVCEWGPSTSLTT-----KAVLLVRKFQNSPAEDFQPCQY 167
Qy 171 --PODPLGAARCVVHGAEFWSQYRINVTENPLGAS--TRLLDVSLSQILRPDPPOGLRVE 227
Db 168 SOESQKFCQLAVPEGDS--SFYIVSMCVASSVSGSKFSTQTFCGCGILQDPDPANIIVT 225
Qy 228 SVPGYPRRLRASWTYPASWPCOPHLLKFRLOYRPAQHPAWSTVEPAGLEE--VITDAVA 285
Db 226 AVARNPRWLSVTWQDPHSHWN--SSFYRLRFELRYAERSKTTFTTMVKDLQHHCVIHDWS 284
Qy 286 GLPHAVRYSARDFLDAGTWSTWSPAWGTPTGTTPKEIPAWQLHTQPEVEPQVDSAP 345
Db 285 GLRHVVQLRAQEEFCQGESEWSPEAMGTPWTES--RSPPAENEVSTPMELDPCGYISP 342
Qy 346 PRPSLQPH 353
Db 343 ESPVQLH 350

RESULT 4

US-09-935-868-24
; Sequence 24, Application US/09935868
; Patent No. US20020164690A1

GENERAL INFORMATION:

; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 24

LENGTH: 1168

TYPE: PRT

ORGANISM: Homo sapiens

US-09-935-868-24

Query Match 14.6%; Score 332; DB 9; Length 1168;
Best Local Similarity 30.2%; Pred. No. 1.2e-14;
Matches 114; Conservative 42; Mismatches 161; Indels 60; Gaps 16;

Qy 5 CSGLSRLVAVATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGD--PVSWFRD 62
Db 6 CALLAALLAAPCAAL--APRRCPAQAEVARGVLTSLPGDSVTLTCFGEVEDNATVHW-- 60
Qy 63 GEPKLLQGPD-----SGLGHELVLAQADSTDEGTICQTLGALGGTTLQLGYPPA 114
Db 61 ----VLRKPAAGSHPSRWAGMGRLLRSVLHDSGNTSCYRA--GRPAGTVHLLVDVPE 115
Qy 115 RPVWSC-QAADYENFSCWSPSQISGLPTRYLTSYRKKTVLGADSORSPSTG--PWPC-- 170
Db 116 EPQLSCFRKSPLSNVVCEWGPSTSLTT-----KAVLLVRKFQNSPAEDFQPCQY 167
Qy 171 --PODPLGAARCVVHGAEFWSQYRINVTENPLGAS--TRLLDVSLSQILRPDPPOGLRVE 227
Db 168 SOESQKFCQLAVPEGDS--SFYIVSMCVASSVSGSKFSTQTFCGCGILQDPDPANIIVT 225
Qy 228 SVPGYPRRLRASWTYPASWPCOPHLLKFRLOYRPAQHPAWSTVEPAGLEE--VITDAVA 285
Db 226 AVARNPRWLSVTWQDPHSHWN--SSFYRLRFELRYAERSKTTFTTMVKDLQHHCVIHDWS 284
Qy 286 GLPHAVRYSARDFLDAGTWSTWSPAWGTPTGTTPKEIPAWQLHTQPEVEPQVDSAP-- 343
Db 285 GLRHVVQLRAQEEFCQGESEWSPEAMGTPWTES-----RSPPAENEVSTPMT 332

Qy 344 --APRPSLQPHPRLLD 358
Db 333 GGAPSGAOLE----LLD 345

RESULT 5

US-09-935-868-15
; Sequence 15, Application US/09935868
; Patent No. US20020164690A1

GENERAL INFORMATION:

; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15

LENGTH: 360

TYPE: PRT

ORGANISM: Homo sapiens

US-09-935-868-15

Query Match 14.5%; Score 329.5; DB 9; Length 360;
Best Local Similarity 29.2%; Pred. No. 4.8e-15;

Matches 112; Conservative 46; Mismatches 172; Indels 53; Gaps 15;

Qy 5 CSGLSRLVAVATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGD--PVSWFRD 62
Db 6 CALLAALLAAPCAAL--APRRCPAQAEVARGVLTSLPGDSVTLTCFGEVEDNATVHW-- 60
Qy 63 GEPKLLQGPD-----SGLGHELVLAQADSTDEGTICQTLGALGGTTLQLGYPPA 114
Db 61 ----VLRKPAAGSHPSRWAGMGRLLRSVLHDSGNTSCYRA--GRPAGTVHLLVDVPE 115
Qy 115 RPVWSC-QAADYENFSCWSPSQISGLPTRYLTSYRKKTVLGADSORSPSTG--PWPC-- 170
Db 116 EPQLSCFRKSPLSNVVCEWGPSTSLTT-----KAVLLVRKFQNSPAEDFQPCQY 167
Qy 171 --PODPLGAARCVVHGAEFWSQYRINVTENPLGAS--TRLLDVSLSQILRPDPPOGLRVE 227
Db 168 SOESQKFCQLAVPEGDS--SFYIVSMCVASSVSGSKFSTQTFCGCGILQDPDPANIIVT 225
Qy 228 SVPGYPRRLRASWTYPASWPCOPHLLKFRLOYRPAQHPAWSTVEPAGLEE--VITDAVA 285
Db 226 AVARNPRWLSVTWQDPHSHWN--SSFYRLRFELRYAERSKTTFTTMVKDLQHHCVIHDWS 284
Qy 286 GLPHAVRYSARDFLDAGTWSTWSPAWGTPTGTTPKEIPAWQLHTQPEVEPQVDSAP 345
Db 285 GLRHVVQLRAQEEFCQGESEWSPEAMGTPWTES-----RSPPAENEVSTPMTQ 332
Qy 346 PRPSLQPHPRLLDHRDSVEQVAV 368
Db 333 ALTTNKDDNLL-PRDSANATSL 354

RESULT 6

US-09-935-868-8
; Sequence 8, Application US/09935868
; Patent No. US20020164690A1

GENERAL INFORMATION:

; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 8

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; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-8

Query Match      14.5%; Score 329.5; DB 9; Length 592;
Best Local Similarity 29.2%; Pred. No. 8.4e-15;
Matches 112; Conservative 46; Mismatches 172; Indels 53; Gaps 15;

QY 5 CSGLSRVLAVATALVASSPCQAWPGVQYQPGGRSVKLCQPGVTAGD--PVSWFRD 62
Db 6 CALLAALLAAPGAAL--APRCRPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW--- 60

QY 63 GEPKLLQGPD-----SGLGHELVLAQADSTDEGTYYICOTLDGALGGTTLQLGYPPA 114
Db 61 ---VLRKPAAGSHPSRWAGMGRLLRSVLQHDGNGVSCYRA-GRPAGTVHLLVDVPPE 115

QY 115 RPVVSC--QAADYENFSCWSPSQISGLPTRYLTYSRKTKTVLGADSQRRSPSTG--PWPC-- 170
Db 116 EPQLSCFRKSPLSNVVCEWGPSTPSLTT-----KAVLLVRKFQNSPAEDFQEPCCY 167

QY 171 --PQDPLGAARCVVHGAEFWSQYRINTEVYNPLGAS--TRLLDVSLSQILRDPDPQGLRVE 227
Db 168 SQESQKSCQAVPEGDS--SFYIVSMCVASSVGSKFSKQTQFGCGGILQDPDPANITVT 225

QY 228 SVPGYPRRLRASWTYPASWPCQPHFLKFRLYRPAQHAWSTVEPAGLEE--VITDAVA 285
Db 226 AVARNRWLSVTQDPHSWN--SSFYRLRFELRYRAERSKFTTTMMVKDLQHHCVIHDWS 284

QY 286 GLPHAVRSARDFLDAGTWSPSEANGTPTSTGTPKREIPAWGQLHTQPEVQDVSPAP 345
Db 285 GLRHVVQLRAQEEFGQGEWSPEAMGTPTWES-----RSPPAENEVSTPMQ 332

QY 346 PRPSLOPHRLDHRDSVEQAV 368
Db 333 ALTNKDDNLL-PRDSANATSL 354

RESULT 7
US-09-935-868-16
; Sequence 16, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 16
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-16

Query Match      13.8%; Score 315; DB 9; Length 315;
Best Local Similarity 31.0%; Pred. No. 3.8e-14;
Matches 102; Conservative 38; Mismatches 149; Indels 40; Gaps 13;

QY 5 CSGLSRVLAVATALVASSPCQAWPGVQYQPGGRSVKLCQPGVTAGD--PVSWFRD 62
Db 6 CALLAALLAAPGAAL--APRCRPAQEVARGVLTSLPGDSVTLTCPGVEPEDNATVHW--- 60

QY 63 GEPKLLQGPD-----SGLGHELVLAQADSTDEGTYYICOTLDGALGGTTLQLGYPPA 114
Db 61 ---VLRKPAAGSHPSRWAGMGRLLRSVLQHDGNGVSCYRA-GRPAGTVHLLVDVPPE 115

QY 115 RPVVSC--QAADYENFSCWSPSQISGLPTRYLTYSRKTKTVLGADSQRRSPSTG--PWPC-- 170
Db 116 EPQLSCFRKSPLSNVVCEWGPSTPSLTT-----KAVLLVRKFQNSPAEDFQEPCCY 167
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QY 171 --PQDPLGAARCVVHGAEFWSQYRINTEVYNPLGAS--TRLLDVSLSQILRDPDPQGLRVE 227
Db 168 SQESQKSCQAVPEGDS--SFYIVSMCVASSVGSKFSKQTQFGCGGILQDPDPANITVT 225

QY 228 SVPGYPRRLRASWTYPASWPCQPHFLKFRLYRPAQHAWSTVEPAGLEE--VITDAVA 285
Db 226 AVARNRWLSVTQDPHSWN--SSFYRLRFELRYRAERSKFTTTMMVKDLQHHCVIHDWS 284

QY 286 GLPHAVRSARDFLDAGTWSPSEANGT 314
Db 285 GLRHVVQLRAQEEFGQGEWSPEAMGT 313

RESULT 8
US-10-000-776-10
; Sequence 10, Application US/10000776
; Patent No. US20020164609A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Pflanz, Stefan K.-H.
; APPLICANT: Kastelein, Robert A.
; APPLICANT: Bazan, Jose F.
; APPLICANT: Rennick, Donna
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Cheung, Jeanne
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX01040K3
; CURRENT APPLICATION NUMBER: US/10/000,776
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/791,497
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/627,897
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,581
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/147,763
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-776-10

Query Match      11.2%; Score 255.5; DB 9; Length 229;
Best Local Similarity 30.9%; Pred. No. 2.4e-10;
Matches 73; Conservative 35; Mismatches 95; Indels 33; Gaps 10;

QY 94 COTLDGALGGTTLQLGYPPAR---PVVSCQAADYE-NFSCWTS--PSQISGLPTRYLTS 147
Db 15 CPSCSGRKG-----PPAALTLPVQCASRYPIAVDCSWTLPAPNSTSPVSIAT 65

QY 148 YRKTVLGADSQRRSPSTGWPCCQDPLGAARCVVHGAEFWSQ--YRINTEVYNPLGAST 205
Db 66 YR----LGMARHGS-----WPCLLQQTPTSTCTITDQLFMSAPYVLNVTAHVHWSGS 116

QY 206 RLDDVSLSQILRDPDPQGLRVESVPGYPRRLRASWTYPASWPCQPHFLKFRLYRPAQH 265
Db 117 SFVPFTTEHIKIPDPPEGVRLS---PLAERHVQVQVQVQVQVQVQVQVQVQVQVQVQV 174

QY 266 PAWSTVEPAGLEEVIITDAVAGLPHA---VRVSARDFLDAGTWSPSEANGTPTSTG 318
Db 175 ARHRVQPIEATSFILRAVR--PRARYVQVAAQDLTDYGLSDSLPATATMSLG 228

RESULT 9
US-09-791-497-12
; Sequence 12, Application US/09791497
; Publication No. US20030008343A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
```

APPLICANT: Kastelein, Robert A.
APPLICANT: Bazan, J. Fernando
APPLICANT: Pfanz, Stefan
TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
FILE REFERENCE: DX01040K2
CURRENT APPLICATION NUMBER: US/09/791,497
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 09/627,897
PRIOR FILING DATE: 2000-07-27
PRIOR APPLICATION NUMBER: 60/146,581
PRIOR FILING DATE: 1999-07-30
PRIOR APPLICATION NUMBER: 60/147,763
PRIOR FILING DATE: 1999-08-06
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 229
TYPE: PRT
ORGANISM: Homo sapiens
US-09-791-497-12

Query Match 11.2%; Score 255.5; DB 9; Length 229;
Best Local Similarity 30.9%; Pred. No. 2.4e-10;
Matches 73; Conservative 35; Mismatches 95; Indels 33; Gaps 10;
QY 94 CQTLDCALGGTTLQLGVPAPR---PVVSCQAADYE-NFSCWTWS--PSQISGLPTRYLTS 147
DB 15 CPFCGRKG-----PPAALTLPVQCRASTRPIADCSWTLPAPNSTRPSVSTAT 65
QY 148 YRKKTVLGADSORSPSTGPNPCQDPLGAARCVVHGAEFWSQ--YRINVTVEVNPGLGAST 205
DB 66 YR---LGMARHGS-----WPCLOQTPSTSTCTTDVQLFSMAFYVLNVTAVHPWGSSS 116
QY 206 RLIDVSLQSLRPDPQGLRVESVPGYPRRLRASVTYFASWPCQPHFLKFLRLQYRPAQH 265
DB 117 SVVPFTEHIIKPDPEGVRLS--PLAEHVQVQVEPPGSPFPFIFSLKYWIRYKROGA 174
QY 266 PAWSTVEPAGLEVTIDTAVAGLUPHA---VRVSARDFLDAGTWTSTWSPAWGTPSTG 318
DB 175 ARFHRVGPIEATSFILRAVR--PRARYVQVAAQDLTDYGELSDMSLPATATMSLG 228

RESULT 10
US-09-880-578-27
Sequence 27, Application US/09880578
Patent No. US20020045733A1

GENERAL INFORMATION:
APPLICANT: Lok, Si
Presnell, Scott R.
Jelmeberg, Anna C.
Gilbert, Teresa
Foster, Donald C.
Adams, Robyn L.
Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,578
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lunn, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-880-578-27

Query Match 9.3%; Score 212.5; DB 10; Length 389;
Best Local Similarity 23.8%; Pred. No. 3e-07;
Matches 89; Conservative 54; Mismatches 136; Indels 95; Gaps 19;
QY 17 TALVSASSPCQAWGPPGVGYGPGRSVKLC-----PGVTAGDPVSWFRDGE---PKL 67
DB 3 TAVISPDQPTLLI-----GSSLATCSVHGDPGATA-EGLYWTLNGRRLLPPEL 50
QY 68 LOGPSGGLGHELVLAQAD-----STDEGYICQTLGALGGTVTLQGLYPPARPV-VSQO 121
DB 51 SRVLNAS---LALALANLNGSRQSGDNLVCHARDGSLAGSCLYVGLPPEKPVNISCW 107
QY 122 ADYENFSCWTSPSQ--ISGLPTRYLTSYRKKTIVLGAQDSQRRSPSTGPNPC--PODPLCA 177
DB 108 SKNMKDLTCRWTPGAGHGETFLHTNYSKYLKRWYGODNCEBYHTVGPCHSHIPKD----- 163
QY 178 ARCVVHGAEFWSQYRINVTVEVNPGLAS--TRLDDVSLQSLRPDPQGLRVESVPGYPRRL 236
DB 164 -----LALFPYEIWEATNRLGSSRSDVLTLDLDVVTDDPPDPVHVRVGGLEDOL 216
QY 237 RASWTYPSWPCQPHFL--KFRLOYRPAQHPAWSTVEP-----AGLEEVITDAVA 285
DB 217 SVRWVSP---PALKDFLFOAKYQIRYVEDSVDMKVDDVDSNQTSCRLAGLK-----P 266
QY 286 GLPHAVRVVSARDF-----LDAGTWTWS-PEA-----WCTPSTGTI 320
DB 267 GTVYFVQVRCNPFYIGYSGKAGIWSHPTAASTRSRPRPGPGGACPRGGEPSGPV 326
QY 321 PKEIP---AWGOLH 331
DB 327 RRELKQFLGWLAKH 340

RESULT 11
US-09-880-578-24
Sequence 24, Application US/09880578
Patent No. US20020045733A1
GENERAL INFORMATION:
APPLICANT: Lok, Si
Presnell, Scott R.
Jelmeberg, Anna C.
Gilbert, Teresa
Foster, Donald C.
Adams, Robyn L.
Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTORS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
STATE: WA
COUNTRY: USA

ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,578
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lund, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-880-578-24

Query Match 9.3%; Score 211.5; DB 10; Length 389;
Best Local Similarity 23.8%; Pred. No. 3.5e-07;
Matches 89; Conservative 53; Mismatches 137; Indels 95; Gaps 19;

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QY 17 TALVSASPCQAWPGVQVQGPGRSVKLC-----PGVTAGDPVSWFRDGE---PKL 67
Db 3 TAVISPDQPTLLI-----GSSLLATCSVHGDPGATA-EGLYWTNLGRRLPPEL 50
QY 68 LOGPDSGLGHELVLAQAD-----STDEGTYICQTLDGALGCTVTLQGYPPARPV-VSCQ 121
Db 51 SRVLNAS---TLALANLNGSRORSNDLVCHARDGSILAGSCLYVGLPEKPVNISCW 107
QY 122 AADYENFSCWSPSQ--ISGLPTRLYTSYRKKTVLGADSRSPSTGPWPC--PQDPLGA 177
Db 108 SKNMKDLTCRWTPGSHGETFLHTNYSKYLKRWYGQDNTCEEYHTVGPCHSHPKD--- 163
QY 178 ARCVMHGAEFWSQYRINVTENVPLG-ASTRLLDVLSQILRPDPQGLRVESVPGYPRRL 236
Db 164 -----LALFTPEIWEATNRLGSARSVDLTLDILDVVTTPDPPDVHVSRVGGLEDQL 216
QY 237 RASWTPASWPCQPHFL--KFRLOYRPAQHAPWSTVEP-----AGLEEVITDAVA 285
Db 217 SVRWSP---PALKDFLFQAKYQIRYRVESVDWKVVDVSNQTSCLRLAGLK-----P 266
QY 286 GLPHAVRSARDF-----LDAGTWSTWS-PEA-----WGTPSTGTI 320
Db 267 GTVVFQVRCNPFGIYGSKKAGIWESENHPTAASPRSRPGGGACPRGGEPSSGPV 326
QY 321 PKEIP---ANGQLH 331
Db 327 RRELKQFLGLWKKH 340
```

RESULT 12

US-09-880-578-29
Sequence 29, Application US/09880578
Patent No. US2002004573A1
GENERAL INFORMATION:
APPLICANT: Lok, Si
Preenell, Scott R.
Jelmsberg, Anna C.
Gilbert, Teresa

Poster, Donald C.
Adams, Robyn L.
Lehner, Joyce M.
TITLE OF INVENTION: MAMMALIAN ZCYTOR5
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zymogenetics
STREET: 1201 Eastlake Ave East
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/880,578
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Lund, Paul G
REGISTRATION NUMBER: 32,743
REFERENCE/DOCKET NUMBER: 96-22
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-442-6627
TELEFAX: 206-442-6678
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 389 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 29:
US-09-880-578-29

Query Match 9.3%; Score 211.5; DB 10; Length 389;
Best Local Similarity 24.1%; Pred. No. 3.5e-07;
Matches 90; Conservative 52; Mismatches 137; Indels 95; Gaps 19;

```
QY 17 TALVSASPCQAWPGVQVQGPGRSVKLC-----PGVTAGDPVSWFRDGE---PKL 67
Db 3 TAVISPDQPTLLI-----GSSLLATCSVHGDPGATA-EGLYWTNLGRRLPPEL 50
QY 68 LOGPDSGLGHELVLAQAD-----STDEGTYICQTLDGALGCTVTLQGYPPARPV-VSCQ 121
Db 51 SRVLNAS---TLALANLNGSRORSNDLVCHARDGSILAGSCLYVGLPEKPVNISCW 107
QY 122 AADYENFSCWSPSQ--ISGLPTRLYTSYRKKTVLGADSRSPSTGPWPC--PQDPLGA 177
Db 108 SKNMKDLTCRWTPGSHGETFLHTNYSKYLKRWYGQDNTCEEYHTVGPCHSHPKD--- 163
QY 178 ARCVMHGAEFWSQYRINVTENVPLG-ASTRLLDVLSQILRPDPQGLRVESVPGYPRRL 236
Db 164 -----LALFTPEIWEATNRLGSARSVDLTLDILDVVTTPDPPDVHVSRVGGLEDQL 216
QY 237 RASWTPASWPCQPHFL--KFRLOYRPAQHAPWSTVEP-----AGLEEVITDAVA 285
Db 217 SVRWSP---PALKDFLFQAKYQIRYRVESVDWKVVDVSNQTSCLRLAGLK-----P 266
QY 286 GLPHAVRSARDF-----LDAGTWSTWS-PEA-----WGTPSTGTI 320
Db 267 GTVVFQVRCNPFGIYGSKKAGIWESENHPTAASPRSRPGGGACPRGGEPSSGPV 326
QY 321 PKEIP---ANGQLH 331
Db 327 RRELKQFLGLWKKH 340
```



```

: GENERAL INFORMATION:
: APPLICANT: Baker, Kevin
: APPLICANT: Botstein, David
: APPLICANT: Eaton, Dan
: APPLICANT: Ferrara, Napoleone
: APPLICANT: Filvaroff, Ellen
: APPLICANT: Gerritsen, Mary
: APPLICANT: Goddard, Audrey
: APPLICANT: Godowski, Paul
: APPLICANT: Grimaldi, Christopher
: APPLICANT: Gurney, Austin
: APPLICANT: Hillan, Kenneth
: APPLICANT: Kljavin, Ivar
: APPLICANT: Napier, Mary
: APPLICANT: Roy, Margaret
: APPLICANT: Tumas, Daniel
: APPLICANT: Wood, William
: TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
: TITLE OF INVENTION: ACIDS ENCODING THE SAME
: FILE REFERENCE: P2348PIC1
: CURRENT APPLICATION NUMBER: US/09/944,413
: CURRENT FILING DATE: 2001-09-26
: PRIOR APPLICATION NUMBER: 09/866,028
: PRIOR FILING DATE: 2001-05-25
: PRIOR APPLICATION NUMBER: 60/067,411
: PRIOR FILING DATE: December 3, 1997
: PRIOR APPLICATION NUMBER: 60/069,334
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,335
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,278
: PRIOR FILING DATE: December 11, 1997
: PRIOR APPLICATION NUMBER: 60/069,425
: PRIOR FILING DATE: December 12, 1997
: PRIOR APPLICATION NUMBER: 60/069,696
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,694
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,702
: PRIOR FILING DATE: December 16, 1997
: PRIOR APPLICATION NUMBER: 60/069,870
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/069,873
: PRIOR FILING DATE: December 17, 1997
: PRIOR APPLICATION NUMBER: 60/068,017
: PRIOR FILING DATE: December 18, 1997
: PRIOR APPLICATION NUMBER: 60/070,440
: PRIOR FILING DATE: January 5, 1998
: PRIOR APPLICATION NUMBER: 60/074,086
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/074,092
: PRIOR FILING DATE: February 9, 1998
: PRIOR APPLICATION NUMBER: 60/075,945
: PRIOR FILING DATE: February 25, 1998
: PRIOR APPLICATION NUMBER: 60/112,850
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 60/113,296
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 60/146,222
: PRIOR FILING DATE: July 28, 1999
: PRIOR APPLICATION NUMBER: PCT/US98/19330
: PRIOR FILING DATE: September 16, 1998
: PRIOR APPLICATION NUMBER: PCT/US98/25108
: PRIOR FILING DATE: December 1, 1998
: PRIOR APPLICATION NUMBER: 09/216,021
: PRIOR FILING DATE: December 16, 1998
: PRIOR APPLICATION NUMBER: 09/218,517
: PRIOR FILING DATE: December 22, 1998
: PRIOR APPLICATION NUMBER: 09/254,311
: PRIOR FILING DATE: March 3, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/12252
: PRIOR FILING DATE: June 22, 1999
: PRIOR APPLICATION NUMBER: PCT/US99/21090

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PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313
PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28301
PRIOR FILING DATE: December 1, 1999
PRIOR APPLICATION NUMBER: PCT/US99/30095
PRIOR FILING DATE: December 16, 1999
PRIOR APPLICATION NUMBER: PCT/US00/03565
PRIOR FILING DATE: February 11, 2000
PRIOR APPLICATION NUMBER: PCT/US00/04414
PRIOR FILING DATE: February 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/05841
PRIOR FILING DATE: March 2, 2000
PRIOR APPLICATION NUMBER: PCT/US00/08439
PRIOR FILING DATE: March 30, 2000
PRIOR APPLICATION NUMBER: PCT/US00/14042
PRIOR FILING DATE: May 22, 2000
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: July 28, 2000
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: December 1, 2000
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: February 28, 2001
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 32
LENGTH: 422
TYPE: PRT
ORGANISM: Homo Saplen
US-09-944-413-32

Query Match 9.3% Score 211.5; DB 9; Length 422;
Best Local Similarity 23.7%; Pred No. 3.9e-07;
Matches 91; Conservative 53; Mismatches 145; Indels 95; Gaps 19;

QY 7 GLSRVLVAVATALVSASSPCQAWGPGVQVGPGRSVKLC-----PGVTAGDPVSWF 60
Db 30 GAPRAGSGAHTAVISPDQPTLLI-----GSSILATCSVHGPPPGATA-EGLYWT 77
QY 61 RDGE---PKLLOGDPSGLGHELVLAQAD-----STDGTYICQLDGAALGGTVTLQGY 112
Db 78 LNGRRLEPESRVLNLS-----TLALANLNGSRQSRGDNLVCHARDGSILAGSLCYVGLP 134
QY 113 PARPV-VSCOAADYENFSWTSQSPQ--ISGLPRLYLSYRKKTVLGADSORRSPSTGFWP 169
Db 135 PEKPVNISCSKNNKDLTCWTPGAHGETFLHTNYSKYLKRWYQDNTCEEYHTVGP 194
QY 170 C--PQDPLGAARCVVHGAETWQYRINVTNPLG--ASTRLDVSLSQILRPDPQGLRV 226
Db 195 CHPKD-----LALFTPEIWEATNRLGARSVDVLTLDLDVVTTDPPDPVHV 243
QY 227 ESNVGPYRRLRASWTYTPASWPCQPHFL--KFRLOYRPAQHPANSTVEP-----AG 275
Db 244 SRVGLEDQLSVRWVSP---PALKDFLQAKYQIRYVEDSDVMKVVDDVSNQTSCLAG 300
QY 276 LEEVITDAVAGLPHAVRVSARDF-----LDAGTWSTWS-PEA----- 311
Db 301 LK-----PGTVYFVQVRCNPGIYSGKAGIWSHPTAASPRSRPGRPGGGACEP 353
QY 312 -WGPSTGTIPKEIP---AWGOLH 331
Db 354 RGGEPSSGPVRRELKQFLGWLK 377

RESULT 15

US-09-944-403-32
Sequence 32, Application US/09944403
Patent No. US20020165143A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan

APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kijavlin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,403
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 60/146,222
PRIOR FILING DATE: July 28, 1999
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/25108
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090
PRIOR FILING DATE: September 15, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28409
PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
PRIOR APPLICATION NUMBER: PCT/US99/28313

;; PRIOR FILING DATE: No. US20020165143A1ember 30, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/28301
;; PRIOR FILING DATE: December 1, 1999
;; PRIOR APPLICATION NUMBER: PCT/US99/30095
;; PRIOR FILING DATE: December 16, 1999
;; PRIOR APPLICATION NUMBER: PCT/US00/03565
;; PRIOR FILING DATE: February 11, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/04414
;; PRIOR FILING DATE: February 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/05841
;; PRIOR FILING DATE: March 2, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/08439
;; PRIOR FILING DATE: March 30, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/14042
;; PRIOR FILING DATE: May 22, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/20710
;; PRIOR FILING DATE: July 28, 2000
;; PRIOR APPLICATION NUMBER: PCT/US00/32678
;; PRIOR FILING DATE: December 1, 2000
;; PRIOR APPLICATION NUMBER: PCT/US01/06520
;; PRIOR FILING DATE: February 28, 2001
;; NUMBER OF SEQ ID NOS: 120
;; SEQ ID NO 32
;; LENGTH: 422
;; TYPE: PRT
;; ORGANISM: Homo Sapien
US-09-944-403-32

Query Match 9.3%; Score 211.5; DB 9; Length 422;
Best Local Similarity 23.7%; Pred. No. 3.9e-07;
Matches 91; Conservative 53; Mismatches 145; Indels 95; Gaps 19;

Qy 7 GLSRVLVAVATLVASSPCQAWPGVQYQDGRSVKLC-----PGVTAGDPVSWF 60
Db 30 GAPRAGSAHTAVISPDPTLLI-----GSSLATCSVHGDPGATA-EGLYWT 77

Qy 61 RDGE---PKLLQGPSGLGHELVLAQAD-----STDEGTICQTLDGALGGTVTTLQLGYP 112
Db 78 LNGRLPPPELSRVLNAS---TLALANLNGSRQSRGDNLYCHARDGSILAGSCLYVGLP 134

Qy 113 PARPV-VSCQADYENFCTWSPSQ--ISGLPTRYLTYSRKKTVLGADSQRRSPSTGPWP 169
Db 135 PEKPVNISCSKMKDLRCRWTPGAHGETFLHTNYSKYLKRWYQDNTCEYHTVGPMS 194

Qy 170 C--PODPLGAARCVVHGAFFWFOYRINVTYNPLG-ASTRLDVSLSQILRPDPQGLRV 226
Db 195 CHIPKD-----LALFTPYEIWENRUGSARSDVLTLDILDVTTDPPDVHV 243

Qy 227 ESVGYPRLRASWTYPASWPCQPHLL--KFRQYRPAQHPANSTVEP-----AG 275
Db 244 SRVGGLEDQLSVRWVSP---PALKDFLQAKYQIRYVEDSDVKVDDVSNQTSCLAG 300

Qy 276 LEEVITDAVGLPHAVRVARSADF-----LDAGTWTWS-PEA-----311
Db 301 LK-----PGTVYFVQVRCNPFYIGSKKAGINSEWSHPTAASPRSERPGPGGACPE 353

Qy 312 -WGTPSTGTIPKEIP--AWQLH 331
Db 354 RGEPPSGPVRRELKQFLGLWKKH 377

Search completed: January 17, 2003, 19:40:18
Job time : 17 secs

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GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:36:45 ; Search time 18 seconds
(without alignments)
689.804 Million cell updates/sec

Title: US-09-924-338-2

Perfect score: 2275

Sequence: 1 MSSSCSGLSRVLVAVATALV.....KPGFLASVIVDRRCPAPNL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*

- 1: /cgn2.6/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgn2.6/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgn2.6/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgn2.6/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgn2.6/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgn2.6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2275	100.0	422	4	US-09-151-102-2
2	2275	100.0	422	4	US-08-929-846-2
3	2257.5	99.2	423	4	US-08-702-665A-5
4	1897	83.4	432	4	US-08-702-665A-3
5	1831	80.5	441	4	US-09-151-102-4
6	1831	80.5	441	4	US-08-929-846-4
7	382	16.8	372	4	US-09-211-590-2
8	379	16.7	372	1	US-07-865-878A-4
9	379	16.7	372	1	US-07-676-647-2
10	379	16.7	372	1	US-08-449-329-2
11	379	16.7	372	2	US-08-445-073-2
12	379	16.7	372	2	US-08-585-258-2
13	379	16.7	372	2	US-08-603-010-4
14	379	16.7	372	5	PCT-US91-03896-2
15	360	15.8	468	4	US-08-795-473B-5
16	360	15.8	468	4	US-09-439-856-5
17	360	15.8	468	6	5171840-2
18	360	15.8	468	6	5480796-2
19	330	14.5	344	6	5171840-7
20	330	14.5	344	6	5480796-7
21	325	14.3	323	6	5171840-6
22	325	14.3	323	6	5480796-6
23	259.5	11.4	229	2	US-08-684-687-2
24	259.5	11.4	229	3	US-08-352-678-6
25	255.5	11.2	229	1	US-08-383-750-6
26	240	10.5	230	5	PCT-US93-09636-6
27	232	10.2	386	6	5171840-5

28	232	10.2	386	6	5480796-5	Patent No. 5480796
29	221	9.7	210	4	US-09-043-785-1	Sequence 1, Appli
30	212.5	9.3	389	4	US-09-071-224-27	Sequence 27, Appli
31	211.5	9.3	389	4	US-09-071-224-24	Sequence 24, Appli
32	211.5	9.3	389	4	US-09-071-224-29	Sequence 29, Appli
33	211.5	9.3	425	4	US-09-071-224-4	Sequence 4, Appli
34	210.5	9.3	389	4	US-09-071-224-22	Sequence 22, Appli
35	210.5	9.3	389	4	US-09-071-224-25	Sequence 25, Appli
36	210.5	9.3	389	4	US-09-071-224-26	Sequence 26, Appli
37	210.5	9.3	389	4	US-09-071-224-30	Sequence 30, Appli
38	210.5	9.3	392	4	US-09-071-224-18	Sequence 18, Appli
39	210.5	9.3	422	4	US-09-071-224-2	Sequence 2, Appli
40	209.5	9.2	389	4	US-09-071-224-28	Sequence 28, Appli
41	209.5	9.2	405	3	US-09-012-072-2	Sequence 2, Appli
42	209.5	9.2	405	4	US-09-120-601-2	Sequence 2, Appli
43	207.5	9.1	303	4	US-09-071-224-23	Sequence 23, Appli
44	207.5	9.1	385	4	US-09-071-224-19	Sequence 19, Appli
45	207.5	9.1	385	4	US-09-071-224-20	Sequence 20, Appli

ALIGNMENTS

RESULT 1
US-09-151-102-2
; Sequence 2, Application US/09151102
; Patent No. 6274547
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 Cambridgepark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/151,102
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/663,584
; FILING DATE: 14-JUN-1996
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-151-102-2

Query Match 100.0%; Score 2275; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.4e-173;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MSSSCSGLSRVLVAVATALVSASSPCQAMGPPGVQVQGPGRSVKLCPCGVGTAGDPVSWF 60
|||||

Db 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQOPGRSVKLCPCGVTAGDPVSWF 60
QY 61 RDGEKLLQGGPSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQGLYPPARPVYSC 120
Db 61 RDGEKLLQGGPSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQGLYPPARPVYSC 120
QY 121 QAADYENFSCWSPSQISGLPTRYLTYSYRKKTVLGDQSRRSPSTGWPCCQDPLGAARC 180
Db 121 QAADYENFSCWSPSQISGLPTRYLTYSYRKKTVLGDQSRRSPSTGWPCCQDPLGAARC 180
QY 181 VVHGAEFWSQYRINVTENPLGASTRLLDVSLQSTLRDPDQGLRVESVPCYPRRLRASW 240
Db 181 VVHGAEFWSQYRINVTENPLGASTRLLDVSLQSTLRDPDQGLRVESVPCYPRRLRASW 240
QY 241 TYPASWPCQPHFLKFRLOYRPAQHPAWSTVEPAGLVEEITDAVAGLPHAVRVASRDFLD 300
Db 241 TYPASWPCQPHFLKFRLOYRPAQHPAWSTVEPAGLVEEITDAVAGLPHAVRVASRDFLD 300
QY 301 AGTWSTWSPCAWGTPTGTTPKEIPANGQLHTQPEVEPQVDSAPPRLSLQPHPRLLDHR 360
Db 301 AGTWSTWSPCAWGTPTGTTPKEIPANGQLHTQPEVEPQVDSAPPRLSLQPHPRLLDHR 360
QY 361 DSVEQVAVLASGLTSLFGLVAGALALGLWLRRLRGKDGSPKPGFLASVIPVDRRPGAP 420
Db 361 DSVEQVAVLASGLTSLFGLVAGALALGLWLRRLRGKDGSPKPGFLASVIPVDRRPGAP 420
QY 421 NL 422
Db 421 NL 422

RESULT 2

US-08-929-846-2
; Sequence 2, Application US/08929846
; Patent No. 6350855
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,846
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/563,584
; FILING DATE: 14-JUN-1996
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: G15252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5851
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-929-846-2

Query Match 100.0%; Score 2275; DB 4; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.4e-173;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQOPGRSVKLCPCGVTAGDPVSWF 60
Db 1 MSSCSGLSRVLVAVATALVSASSPCQAWGPPGVQYQOPGRSVKLCPCGVTAGDPVSWF 60
QY 61 RDGEKLLQGGPSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQGLYPPARPVYSC 120
Db 61 RDGEKLLQGGPSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQGLYPPARPVYSC 120
QY 121 QAADYENFSCWSPSQISGLPTRYLTYSYRKKTVLGDQSRRSPSTGWPCCQDPLGAARC 180
Db 121 QAADYENFSCWSPSQISGLPTRYLTYSYRKKTVLGDQSRRSPSTGWPCCQDPLGAARC 180
QY 181 VVHGAEFWSQYRINVTENPLGASTRLLDVSLQSTLRDPDQGLRVESVPCYPRRLRASW 240
Db 181 VVHGAEFWSQYRINVTENPLGASTRLLDVSLQSTLRDPDQGLRVESVPCYPRRLRASW 240
QY 241 TYPASWPCQPHFLKFRLOYRPAQHPAWSTVEPAGLVEEITDAVAGLPHAVRVASRDFLD 300
Db 241 TYPASWPCQPHFLKFRLOYRPAQHPAWSTVEPAGLVEEITDAVAGLPHAVRVASRDFLD 300
QY 301 AGTWSTWSPCAWGTPTGTTPKEIPANGQLHTQPEVEPQVDSAPPRLSLQPHPRLLDHR 360
Db 301 AGTWSTWSPCAWGTPTGTTPKEIPANGQLHTQPEVEPQVDSAPPRLSLQPHPRLLDHR 360
QY 361 DSVEQVAVLASGLTSLFGLVAGALALGLWLRRLRGKDGSPKPGFLASVIPVDRRPGAP 420
Db 361 DSVEQVAVLASGLTSLFGLVAGALALGLWLRRLRGKDGSPKPGFLASVIPVDRRPGAP 420
QY 421 NL 422
Db 421 NL 422

RESULT 3

US-08-702-665A-5
; Sequence 5, Application US/08702665A
; Patent No. 6274708
; GENERAL INFORMATION:
; APPLICANT: Hilton, Douglas J.
; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States of America
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/702,665A
; FILING DATE: 20-DEC-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Presser, Leopold
; REGISTRATION NUMBER: 19,827
; REFERENCE/DOCKET NUMBER: 10296
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:

LENGTH: 423 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-665A-5

Query Match 99.2%; Score 2257.5; DB 4; Length 423;
Best Local Similarity 99.5%; Pred. No. 3.5e-172;
Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 MSSSCGLSRVLAVATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSWF 60
DB 1 MSSSCGLSRVLAVATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSWF 60
QY 61 RGEKLLQGPDSGLGHELVLAQADSTDEGTICQTLGALGCTVTLQIGYPPARPVWSC 120
DB 61 RGEKLLQGPDSGLGHELVLAQADSTDEGTICQTLGALGCTVTLQIGYPPARPVWSC 120
QY 121 QAADYENFCTWSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGPPCQDPLGAARC 180
DB 121 QAADYENFCTWSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGPPCQDPLGAARC 180
QY 181 VHGAEFWSQYRINVTENVPL-GASTRLLDVLSQSLRDPDPOGLRVESVPGYPRRLRAS 239
DB 181 VHGAEFWSQYRINVTENVPLGASTRLLDVLSQSLRDPDPOGLRVESVPGYPRRLRAS 240
QY 240 WTPASWPCQPHFLKFRQYRPAQHPAWSTVEPAGLEEVITDVAAGLPHAVRVSADEL 299
DB 241 WTPASWPCQPHFLKFRQYRPAQHPAWSTVEPAGLEEVITDVAAGLPHAVRVSADEL 300
QY 300 DAGTWTWSPEAWGTSTGTIPKEIPAWQLHTQPEVEQVDSPPAPRPSLOPHRLLDH 359
DB 301 DAGTWTWSPEAWGTSTGTIPKEIPAWQLHTQPEVEQVDSPPAPRPSLOPHRLLDH 360
QY 360 RDSVEQVAVLASGILSFLGLVAGALALGLWLRGGKDGSPKPGFLASVTPVDRRPGA 419
DB 361 RDSVEQVAVLASGILSFLGLVAGALALGLWLRGGKDGSPKPGFLASVTPVDRRPGA 420
QY 420 PNL 422
DB 421 PNL 423

RESULT 4
US-08-702-665A-3
Sequence 3, Application US/08702665A
Patent No. 6274708

GENERAL INFORMATION:
APPLICANT: Hilton, Douglas J.
TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: United States of America
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/702,665A
FILING DATE: 20-DEC-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Presser, Leopold
REGISTRATION NUMBER: 19,827
REFERENCE/DOCKET NUMBER: 10296
TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366
TELEX: 203 901 SANS UR
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 432 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-702-665A-3

Query Match 83.4%; Score 1897; DB 4; Length 432;
Best Local Similarity 83.5%; Pred. No. 1.9e-143;
Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1;
QY 1 MSSSCGLSRVLAVATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSWF 60
DB 1 MSSSCGLSRVLAVATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSWF 60
QY 61 RGEKLLQGPDSGLGHELVLAQADSTDEGTICQTLGALGCTVTLQIGYPPARPVWSC 120
DB 61 RGEKLLQGPDSGLGHELVLAQADSTDEGTICQTLGALGCTVTLQIGYPPARPVWSC 120
QY 121 QAADYENFCTWSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGPPCQDPLGAARC 180
DB 121 QAADYENFCTWSPSQISGLPTRYLTSYRKKTLPGAESQRESPTGPPCQDPLEASRC 180
QY 181 VHGAEFWSQYRINVTENVPLGASTRLLDVLSQSLRDPDPOGLRVESVPGYPRRLRASW 240
DB 181 VHGAEFWSQYRINVTENVPLGASTRLLDVLSQSLRDPDPOGLRVESVPGYPRRLHAW 240
QY 241 WTPASWPCQPHFLKFRQYRPAQHPAWSTVEPAGLEEVITDVAAGLPHAVRVSADEL 300
DB 241 WTPASWPCQPHFLKFRQYRPAQHPAWSTVEPAGLEEVITDVAAGLPHAVRVSADEL 300
QY 301 AGTWTWSPEAWGTSTGTIPKEIPAWQLHTQ--PEVEQVDSPPAPRPSLOPHRLLD 358
DB 301 AGTWTWSPEAWGTSTGTIPKEIPAWQLHTQ--PEVEQVDSPPAPRPSLOPHRLLD 360
QY 359 HRDSVEQVAVLASGILSFLGLVAGALALGLWLRGGKDGSPKPGFLASVTPVDRRPG 418
DB 361 HRDPEQVAVLASGILSFLGLVAGALALGLWLRGGKDGSPKPGFLASVTPVDRRPG 420
QY 419 APNL 422
DB 421 IPNL 424

RESULT 5
US-09-151-102-4
Sequence 4, Application US/09151102
Patent No. 6274547
GENERAL INFORMATION:
APPLICANT: Tobin, James
TITLE OF INVENTION: HUMAN INTERLUKIN-11 RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/151,102
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/663,584

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,590
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,647
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-211-590-2

Query Match 16.8%; Score 382; DB 4; Length 372;
Best Local Similarity 30.1%; Pred. No. 8.6e-23;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

QY 12 LVAVATALVSASSPCQANGPGVOYQGPCRSVKLCPCGVTAGDPVSWFRDGEPKLLQGP 71
DB 12 VLAAAAYVYQHRSPQE--APHVQYERLGSVDTLPCGTANWDAAVTRVNGTD---LAP 66
QY 72 DSGLGHVLAQADSTDEGTICQTLDG-ALGCTVTLQGLYPPARPVVSQAAADY-ENFS 129
DB 67 DLLNGSQLVHLGLHGLSGLYACFHRDSWHLRHQVLLHVLGPPREPVLSCRSNTYKGFY 126
QY 130 CWTSPSQISGLPT-RYLTYSRKTKTVLGADSRSPSTGPPCPQDPDLGAARCVVHGAEFW 188
DB 127 CSMH-----LPTPTIPNTFNTVTLHSGK-----IMVCEKDPALKNRCHIRYMHLF 172
QY 189 S--OYRINTEVNPLGASTRLDVSILRPPDPOGLRVESVPGYPRRLRASWTYPASW 246
DB 173 STIKYKVSISVSNALGNATAITFDEFTIVKPPENNVARVPSPNRRLEVTWQTPSTW 232
QY 247 PCQPHFLKFRLOYRPAQHPAWSTVEPA-GLEEVITDVAAGLPHAVRVSAARDFDAGTWS 305
DB 233 PDPEFPKFLFRYRPLILDQWQHVELSDGTAHTITDAYAGKEYIIQVAAKD-NEIGTWS 291
QY 306 TWSPEAWGTPSTGTIPKEIPAWQLHTQPEVEQVDSAPPRLSLOPHRLLDHRSVEQ 365
DB 292 DWSVAHAHPTWTEE-PRHLTTEAQ--AAETTTTSTSLAPP-----PTTKICD----- 336
QY 366 VAVLASIGILSFLGLVAGALALGLWLRRLRGKDGSKPKGFLASV 410
DB 337 -----PGEL-----GSGGGSPAPFLVSV 354

RESULT 8
US-07-865-878A-4
Sequence 4, Application US/07865878A
Patent No. 5332672
GENERAL INFORMATION:
APPLICANT: Yancopoulos, George D. et al.
TITLE OF INVENTION: Cell Free Ciliary Neurotrophic
TITLE OF INVENTION: Factor/Receptor Complex
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/865,878A
FILING DATE: 19911202
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/801/562
FILING DATE: 02-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 6526-082
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 8698864/9741
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: AMINO ACID
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-865-878A-4

Query Match 16.7%; Score 379; DB 1; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

QY 12 LVAVATALVSASSPCQANGPGVOYQGPCRSVKLCPCGVTAGDPVSWFRDGEPKLLQGP 71
DB 12 VLAAAAYVYQHRSPQE--APHVQYERLGSVDTLPCGTANWDAAVTRVNGTD---LAP 66
QY 72 DSGLGHVLAQADSTDEGTICQTLDG-ALGCTVTLQGLYPPARPVVSQAAADY-ENFS 129
DB 67 DLLNGSQLVHLGLHGLSGLYACFHRDSWHLRHQVLLHVLGPPREPVLSCRSNTYKGFY 126
QY 130 CWTSPSQISGLPT-RYLTYSRKTKTVLGADSRSPSTGPPCPQDPDLGAARCVVHGAEFW 188
DB 127 CSMH-----LPTPTIPNTFNTVTLHSGK-----IMVCEKDPALKNRCHIRYMHLF 172
QY 189 S--OYRINTEVNPLGASTRLDVSILRPPDPOGLRVESVPGYPRRLRASWTYPASW 246
DB 173 STIKYKVSISVSNALGNATAITFDEFTIVKPPENNVARVPSPNRRLEVTWQTPSTW 232
QY 247 PCQPHFLKFRLOYRPAQHPAWSTVEPA-GLEEVITDVAAGLPHAVRVSAARDFDAGTWS 305
DB 233 PDPEFPKFLFRYRPLILDQWQHVELSDGTAHTITDAYAGKEYIIQVAAKD-NEIGTWS 291
QY 306 TWSPEAWGTPSTGTIPKEIPAWQLHTQPEVEQVDSAPPRLSLOPHRLLDHRSVEQ 365
DB 292 DWSVAHAHPTWTEE-PRHLTTEAQ--AAETTTTSTSLAPP-----PTTKICD----- 336
QY 366 VAVLASIGILSFLGLVAGALALGLWLRRLRGKDGSKPKGFLASV 410
DB 337 -----PGEL-----GSGGGSPAPFLVSV 354

RESULT 9
US-07-676-647-2
Sequence 2, Application US/07676647
Patent No. 5426177
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furth, Mark E.

```

; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/676,647
; FILING DATE: 19910328
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-07-676-647-2

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Query Match          16.7%; Score 379; DB 1; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

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QY 12 LVAVATALVSASSPCQAMGPPGVQYQGPGRSVKLCPCGVTAGDPYSWFRDGEPKLLQGP 71
Db 12 VLAATAAVVYQHRSPQE--APHVQYERLGSVDVTLPCGTANWDAAVTWVNGTD---LAP 66

QY 72 DSGLGHVLAQADSTDEGTTCQTLDG-ALGGTVTLQGYPPARPVVSCQAADY-ENFS 129
Db 67 DLLNGSQLVHLGELHSGLYACFHRDSWHLRHQVLLHVLGPPREPVLSCRSNTYPKGY 126

QY 130 CWSPSQISGLPT-RYLTYSRKTKVLGADSORRSPSTGPPCPQDPLGAARCVVHGAETW 188
Db 127 CSWH-----LPTPTVIPNTVTVLHGSK-----IMVCEKDPALKNRCIHYMHLF 172

QY 189 S--QYRINVTENVPLGASTRLDVSLSQTLRPDPQGLRVESVPGYPRRLRASWTYPASW 246
Db 173 STIKYKVSISVSNALGHNAITATFEFTVKDPDENNVVAVRVPVSNPRLEVWQTPSTW 232

QY 247 PCQPHLLKFRLOYRPAQHPANSTVEPA-GLIEVITDAVAGLPHAVRVASRDLFAGTWS 305
Db 233 PDPESEPLKFFLRPLLDQMHVLSGTAHTITDAYAGKEYIIQVAADK-NEIGTWS 291

QY 306 TWSPEAWGTPSTGTIPKEIPAWGQLHTQPEVPPQVDSPPAPRPSLOPHRLLDHRDSVEQ 365
Db 292 DWSVAHAATPWTEE-PRHLITTEAQ--AAETTTSTSSLAPP-----PTTKICD----- 336

QY 366 VAVLASLGILSLGLVAGALALGLWLRRLRGKDGSKPGFLASV 410
Db 337 -----PGEL-----GSGGGPCAPFLSV 354

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RESULT 10

US-08-449-329-2

; Sequence 2, Application US/08449329

; Patent No. 5648334

; GENERAL INFORMATION:

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; APPLICANT: Davis, Samuel
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Furth, Mark E.
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,329
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/700,677
; FILING DATE: 15-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-449-329-2

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Query Match          16.7%; Score 379; DB 1; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

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QY 12 LVAVATALVSASSPCQAMGPPGVQYQGPGRSVKLCPCGVTAGDPYSWFRDGEPKLLQGP 71
Db 12 VLAATAAVVYQHRSPQE--APHVQYERLGSVDVTLPCGTANWDAAVTWVNGTD---LAP 66

QY 72 DSGLGHVLAQADSTDEGTTCQTLDG-ALGGTVTLQGYPPARPVVSCQAADY-ENFS 129
Db 67 DLLNGSQLVHLGELHSGLYACFHRDSWHLRHQVLLHVLGPPREPVLSCRSNTYPKGY 126

QY 130 CWSPSQISGLPT-RYLTYSRKTKVLGADSORRSPSTGPPCPQDPLGAARCVVHGAETW 188
Db 127 CSWH-----LPTPTVIPNTVTVLHGSK-----IMVCEKDPALKNRCIHYMHLF 172

QY 189 S--QYRINVTENVPLGASTRLDVSLSQTLRPDPQGLRVESVPGYPRRLRASWTYPASW 246
Db 173 STIKYKVSISVSNALGHNAITATFEFTVKDPDENNVVAVRVPVSNPRLEVWQTPSTW 232

QY 247 PCQPHLLKFRLOYRPAQHPANSTVEPA-GLIEVITDAVAGLPHAVRVASRDLFAGTWS 305
Db 233 PDPESEPLKFFLRPLLDQMHVLSGTAHTITDAYAGKEYIIQVAADK-NEIGTWS 291

QY 306 TWSPEAWGTPSTGTIPKEIPAWGQLHTQPEVPPQVDSPPAPRPSLOPHRLLDHRDSVEQ 365
Db 292 DWSVAHAATPWTEE-PRHLITTEAQ--AAETTTSTSSLAPP-----PTTKICD----- 336

QY 366 VAVLASLGILSLGLVAGALALGLWLRRLRGKDGSKPGFLASV 410
Db 337 -----PGEL-----GSGGGPCAPFLSV 354

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Db   292 DWSVAATPWTEE-PRHLTEAQ--AAETTTSTTSLAPP-----PTTKICD----- 336
Qy   366 VAVLASLGILSFLGLVAGALAGLWLRRLRGKDGSPKPGFASV 410
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Db   337 -----PGEL-----GSGGGPCAPPLVSV 354

RESULT 12
US-08-585-258-2
; Sequence 2, Application US/08585258
; Patent No. 5892003
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Furth, Mark E.
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/585,258
; FILING DATE: 11-JAN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/001,904
; FILING DATE:
; APPLICATION NUMBER: US/07/700,677
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-585-258-2

Query Match          16.7%; Score 379; DB 2; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps

Qy   12 LVAVATALVSASSPCCPAWGPPGVQYQGPKSRVKLCPCGYTAGDVSWFRDGPFKLLQGP 71
      :| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db   12 VLAAAAAIVVAQRHSPOE--APHVQVERLGSDDVTLP CGTANWDAAAVTVRVNGTD---LAP 66

Qy   72 DSGLGHELVLVLAQAADSTDEGTYYICOTLDG-ALGGTVTLQLGYPPARPVVSCAADY-ENFS 129
      :| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db   67 DLLNGSQLVLHGLELGHSGIYACFHRRDSWLHRHQVLLHVLGPPREPLVSCRSNTPYPKGFY 126
      :| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|

Qy   130 CTWSPSQISGLPT-RYTYSYRKKTIVLCADSORRSPSTGWPCCPDPLGAARCVMVHGAEFW 188
      |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db   127 CSWH-----LPTPTYIPNTFNVTLVHSGK-----IWCEKDPAKNKRCHIRYMHLF 172
      |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|

Qy   189 S--QYRINTEVNPLGASTRLLLDYSLQSILRPDPQGLRVESPGYPRRLRASWTYPASW 246
      |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|

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QY 130 CTWSPSISGLPT-RYLTSYRKTKTIGADSQRRSPSTGTPCQDPLGAARCVVHGAEFW 246
   !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !:
Db 127 CSMW-----LPTPTYIPNTFNVTLHGSK-----IMWCEKDPALKNRCHIRYWHLF 172

QY 189 S--QYRINVTVEPNLGASTRLLDVSLSQSIILRPPDPQOGLRVESVPGYPRRLRASWITYPASW 246
   !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !:
Db 173 STIKYKVISVSNALGNHATAITFDEFTIIVKPPDPENNVARVPSPNRRLVETWQTPSTM 232

QY 247 PCQPHLLKFLRYRPAQHPAWSTVSPA-GLEEVIITDVAAGLPHAVRVARSARDFLDAGTWS 305
   !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !:
Db 233 PDPEFPFLKFLRYRPLLDQWQHVELSDGTAHTITDAYAGKEYIIQVAAKD-NEIGTWS 291

QY 306 TWSPEANGTSTGTIPKEIPAWQOLHTQPEVEQVDSPPAPRPSLOPHRLDHRDSVEQ 365
   !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !:
Db 292 DWSVAHAHTWTEE-PRHLITEAQ--AAETTTSTTSSLAPP-----PTTKICD----- 336

QY 366 VAVLASGILSFLGLVAGALALGLWLRRLRGKGDKGPKGFLASV 410
   !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !: !:
Db 337 -----PGEL-----GSGGGPCAPFLVSV 354

RESULT 14
PCT-US91-03896-2
; Sequence 2, Application PC/TUS9103896
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel
; APPLICANT: Quinto, Stephen P.
; APPLICANT: Furth, Mark E.
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US91/03896
; FILING DATE: 19910603
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-065-228
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; PCT-US91-03896-2

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Query Match 16.7%; Score 379; DB 5; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;

QY 12 LVAVATALVSASSPCPQAWGPPGYOQPGRSVKLCPCPGVTAGDPVSWFRDGPKEILQGP 71
::: ||| |
Db 12 VLAAAAVVYAQRHSQE-APHQYERLGSVDYLPCTANWDAATWRVNGTD---LAP 66
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QY 72 DSGLGHELVLAQAOSTDEGTICOTLDG-ALGGTVTLQLGPPARPVWSCAANDY-ENFS 12
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Db 67 DLLNGSLVHLGHLGSLVACFRDSDHMLRHQVLLHVGLPPRPVLSCRSNTYPKGFY 126
QY 130 CTWSPSQISGLPT-RYLTSYRKKTVLGADSORRSPSTGPWCPQDPLGAARCVVHGAEFW 188
   :||| : : : ||| :
Db 127 CSWH-----LPTPIYINTFNVTVLHGSK-----IMWCEKDPALKNRCHIRYMLF 172
QY 189 S--QYRINVTENPLGASTRLDVSLSQILRPDPQGLRVESVPGYPRRLRASWTYPASW 246
   :||| : : : ||| :
Db 173 SPIKVKVSVSNALGHNAITTFDEFTIVKPPDPENVVAVRPSNPRRLEVTWQTPSTW 232
QY 247 PCQPHLLKRLQYRPAQHPASTVEPA-GLIEVITDAVAGLPHAVRVSARDFLDAGTWS 305
   :||| : : : ||| :
Db 233 PDPEFPLKFFLURYPLILDOMHVELSDGTAHTITDAYAGKEYTIQVAAD-NEIGTWS 291
QY 306 TWSPEAWGTPTGTIPKEIPAWQLHTQPEVEPQVDSPPAPRPSLQPHRPLLDHRDSVEQ 365
   :||| : : : ||| :
Db 292 DMSVAHAATPWEE-PRHLITEAQ--AAETTTSTTSSLAPP-----PTTKICD----- 336
QY 366 VAVLASLGLSLVAGLALGLMLRLRRGGKDGSPKPGFLASV 410
   :||| : : : ||| :
Db 337 -----PGEL-----GSGGGPCAPFLVSV 354

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RESULT 15

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US-08-795-473B-5
; Sequence 5, Application US/08795473B
; Patent No. 6217858

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GENERAL INFORMATION:

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; APPLICANT: Galun, Ethan
; APPLICANT: Nahot, Orit
; APPLICANT: Blum, Herbert E.
; TITLE OF INVENTION: A Pharmaceutical Composition for Treating
; TITLE OF INVENTION: Hepatitis B Virus (HBV) Infection
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:

```

```

; ADDRESSEE: Davidson, Davidson and Kappel, LLC
; STREET: 1140 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036

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COMPUTER READABLE FORM:

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; MEDIUM TYPE: 3.5 inch disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MS-DOS EDITOR
; CURRENT APPLICATION DATA:

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; APPLICATION NUMBER: US/08/795.473B
; FILING DATE: 11-FEB-1997

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CLASSIFICATION:

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; ATTORNEY/AGENT INFORMATION:
; NAME: Davidson, Clifford M.
; REGISTRATION NUMBER: 32,728
; REFERENCE/DOCKET NUMBER: 963.1007
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)-997-1028
; TELEFAX: (212)-997-1037

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; INFORMATION FOR SEQ ID NO: 5:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 468 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown

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US-08-795-473B-5

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Query Match 15.8%; Score 360; DB 4; Length 468;

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Best Local Similarity 28.4%; Pred. No. 6.6e-21;

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Matches 129; Conservative 57; Mismatches 196; Indels 72; Gaps 19;

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QY 1 MSSCSGSLRVLVAVATLVASSPCQAWGPPGVQYQPGRSVKLCPCGYTAGD--PVS 58
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Db 2 LAVGCALLAALLIAPGAAL--APRCPAQEVARGVITSLPGDSVTLTCPGVEPEDNATVH 59
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QY 59 WFRDGEPKLQCPD-----SGLGHELVLAQAADSTDEGTIVICQTLDGALGGTVTTLQ 110

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Db 60 W-----VLRKPAAGSHPSRWAGMGRLLRLSRVOLHDSGNYSYRA-GRPAGTVHLLVD 111
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QY 111 YPPARPVVSC-QAADYENFSCWTSPQISGLPTRLTYSYRKKTVLGADSORRSPSTG-PW 168
   :||| : : : ||| :
Db 112 VPPEPQLUSCFKRKSLPSNVVCEWGRPSTPSLT-----KAVLLVRKFQNSPAEDFQE 163
QY 169 PC-----PQDPLGAARCVVHGAEFWQYRINVTENVPLGAS-TRLLDVSLSQILRPDPQ 223
   :||| : : : ||| :
Db 164 PCQYSESQKESCOLAVPEGDS--SFYIVSMCVASSVSGSKTQTFOGCGILQDPDPAN 221
QY 224 LRVESVPGYPRRLRASWTYPASWPCQPHLLKFRLOYPQAQHPASTVEPAGLEE--VIT 281
   :||| : : : ||| :
Db 222 ITVTAVARNRPLWSVTWQDPHSWN--SSEYRLRFLRYRAERSKTTTWMVKDLQHHCVTH 280
QY 282 DAVAGLPHAVRVSARDFLDAGTWTSPSEAMGTPTGTIPKEIPAWGOLHTQPEVEPOVD 341
   :||| : : : ||| :
Db 281 DAWSLRHVVQLRAQEEFGQGEWSEWSEAMGTPTWTES-----RSPPAENEVS 328
QY 342 SPAPRPSLQPHRPLLDHRDSVEQVAV-----LASLGLSLFLGLVAGALALG----- 388
   :||| : : : ||| :
Db 329 TPMQALTTNKDDNLL-FRDSANATSLPVQDSSSVPLPTFL-VAGGSLAFGLLCLIAIVL 386
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Job time : 21 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 17, 2003, 19:33:55 ; Search time 41 seconds
(without alignments)
1371.506 Million cell updates/sec

Title: US-09-924-338-2

Perfect score: 2275

Sequence: 1 MSSSCSGLSRVLVAVATALV.....KPGFLASVIVDRRPGPNL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	2275	100.0	422	22	AA936654 Human IL-11 recept
3	2275	100.0	422	22	AAU07725 Human interleukin
4	2275	100.0	422	23	AAE14613 Human interleukin-
5	2257.5	99.2	423	17	AA92814 Human interleukin-
6	1897	83.4	432	17	AA92813 Murine interleukin
7	1871	82.2	432	22	AA936653 Mouse IL-11 recept
8	1831	80.5	441	22	AA990901 Murine Etl-2 gene
9	1831	80.5	441	22	AAU07726 Mouse Etl-2. Mus
10	1831	80.5	441	23	AAE14614 Murine Etl-2 prote

11	1680	73.8	379	21	AAV59390	Murine soluble int
12	771	33.9	257	23	ABB06126	Human NS protein s
13	395.5	17.4	460	13	AA22616	IL-6R for soluble
14	395.5	17.4	460	22	AA36656	Mouse IL-6 recepto
15	382.5	16.8	460	12	AA13318	IL-6 receptor. Mu
16	379	16.7	372	13	AA20024	Ciliary neurotroph
17	379	16.7	372	14	AA37820	Sequence of human
18	379	16.7	372	16	AA370147	Human recombinant
19	378	16.6	349	22	AA63546	Amino acid sequenc
20	363	16.0	468	17	AA98364	Interleukin-6 rece
21	360	15.8	468	10	AA90284	Sequence of a rece
22	360	15.8	468	14	AA37215	IL-6 receptor. Sy
23	360	15.8	468	22	AA36655	Human IL-6 recepto
24	351	15.4	468	10	AA90525	B cell stimulating
25	350	15.4	468	19	AAW71371	Human interleukin-
26	339	14.9	1158	21	AA92205	Fusion polypeptide
27	335.5	14.7	525	18	AA36846	Human fusion polyp
28	332	14.6	1168	21	AA92204	Fusion polypeptide
29	330.5	14.5	543	20	AA03164	Chimeric sIL-6R/IL
30	330	14.5	344	10	AA90528	B cell stimulating
31	330	14.5	345	21	AAV55071	SR345 protein sequ
32	329.5	14.5	360	20	AAW70804	Amino acid sequenc
33	329.5	14.5	360	21	AA92199	Soluble human IL-6
34	329.5	14.5	468	21	AA92196	Human IL-6R-alpha-
35	329.5	14.5	477	21	AA92197	Human IL-6R-alpha-
36	329.5	14.5	592	20	AAW70797	Human interleukin-
37	329.5	14.5	592	21	AA92185	Human IL-6R-alpha-
38	329.5	14.5	690	21	AA92195	Human IL-6R-alpha-
39	325	14.3	326	15	AA58304	Rat ciliary neuro
40	322.5	14.2	515	21	AA15404	IL-6R/IL-6 fusion
41	321	14.1	323	10	AA90527	B cell stimulating
42	316.5	13.9	1042	16	AA970122	IL8-R type 1-GP 1
43	316	13.9	325	21	AA15389	Human interleukin
44	316	13.9	325	21	AA15390	Bovine interleukin
45	315	13.8	315	20	AAW70805	Amino acid sequenc

ALIGNMENTS

RESULT 1

AA990900

ID AA990900 standard; Protein; 422 AA.

XX AA990900;

AC AA990900;

XX 09-OCT-1996 (first entry)

DT Human interleukin-11 receptor.

DE Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

XX Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;

PD 27-JUN-1996.
XX
XX
PF 27-NOV-1995; 95WO-US15400.
XX
PR 22-DEC-1994; 94US-0362304.
XX
PA (GEMY) GENETICS INST INC.
XX
PI Tobin JF;
XX
XX WPI; 1996-309588/31.
DR N-PSDB; AAT33278.
XX
XX New nucleic acid encoding human interleukin 11 receptor - and
PT related protein, antibodies, receptor antagonists, etc, useful for
PT treating and preventing loss-of bone mass
XX
PS Claim 13; Page 35-37; 54pp; English.
XX
CC Human interleukin-11 (IL-11) receptor (AAR99090) is thought to play a
CC role in the regulation of bone maturation and repair. Its amino
CC acid sequence was deduced from a cDNA clone (AAT33278) isolated from
CC a human activated peripheral blood mononuclear cell cDNA library.
CC Recombinant IL-11 receptor or its fragments, pref. amino acids
CC 24-422, 24-365 (soluble extracellular domain), 391-422, 102-422 or
CC 102-365, can be expressed in host cell systems. It is used to
CC treat/prevent loss of bone mass (e.g. osteoporosis, Paget's disease,
CC multiple myeloma or hypogonadal conditions), as well as immune
CC diseases and cancer.
XX
SQ Sequence 422 AA;

Query Match 100.0%; Score 2275; DB 17; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.2e-150;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSCSLSRVLVAVATALVSASSPCQAWPGVQYGPGRSVKLCPCGVTAGDPVSWF 60
Db 1 MSSSCSLSRVLVAVATALVSASSPCQAWPGVQYGPGRSVKLCPCGVTAGDPVSWF 60

QY 61 RGEPEKLLQGPDSGLGHELVLQAADSTDEGTYICQTLDGALGCTVTLQLGYPARPVWSC 120
Db 61 RGEPEKLLQGPDSGLGHELVLQAADSTDEGTYICQTLDGALGCTVTLQLGYPARPVWSC 120

QY 121 QAADYENFSCWTSPSOISGLPTRYLTYSRKKTVLGADSORRSPSTGWPCCQDPLGAARC 180
Db 121 QAADYENFSCWTSPSOISGLPTRYLTYSRKKTVLGADSORRSPSTGWPCCQDPLGAARC 180

QY 181 VHGAEFWQYRINVTENVPLGASTRLLDVLSQISILRPDPQGLRVESVPGYPRRLRASW 240
Db 181 VHGAEFWQYRINVTENVPLGASTRLLDVLSQISILRPDPQGLRVESVPGYPRRLRASW 240

QY 241 TYPASWPCOPHFLLKFRLOYRPAQHPAWSTVEPAGLEEVIDAVAGLPHAVRVASRDFLD 300
Db 241 TYPASWPCOPHFLLKFRLOYRPAQHPAWSTVEPAGLEEVIDAVAGLPHAVRVASRDFLD 300

QY 301 AGTWSTWSPAEANGTPTGTIPKEIPAWGOLHTQPEVEPOVDSPPAPRPSLQHPRLLDHR 360
Db 301 AGTWSTWSPAEANGTPTGTIPKEIPAWGOLHTQPEVEPOVDSPPAPRPSLQHPRLLDHR 360

QY 361 DSVEQVAVLASLIGLSFLGLVAGALALGLWLRGGKDGSPKPGFLASVIPVDRPPGAP 420
Db 361 DSVEQVAVLASLIGLSFLGLVAGALALGLWLRGGKDGSPKPGFLASVIPVDRPPGAP 420

QY 421 NL 422
Db 421 NL 422

RESULT 2
AAB36654
ID AAB36654 standard; Protein; 422 AA.
XX

AC AAB36654;
XX
XX 13-MAR-2001 (first entry)
DE
XX Human IL-11 receptor subunit alpha protein SEQ ID NO:11.
XX
KW DNAX cytokine receptor subunit; DCRS2; receptor protein;
KW modulating cell proliferation; diagnosis; detection; drug screening;
KW immunological disorder.
XX
XX Homo sapiens.
XX
XX WO2000073451-A1.
XX
XX 07-DEC-2000.
XX
XX 30-MAY-2000; 2000WO-US14867.
XX
XX 01-JUN-1999; 99US-0322913.
XX
XX (SCHE) SCHERING CORP.
XX
XX Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
XX
XX WPI; 2001-061536/07.
XX
XX Novel composition comprising DNAX cytokine receptor subunit polypeptide
PT useful for regulating immune system function and for treating
PT immunological disorders -
XX
XX Disclosure; Page 13-15; 93pp; English.
XX
XX The present invention describes a composition (I) comprising a
CC recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide.
CC The DCRS2 polypeptide is useful for binding ligands and for preparing
CC antibodies. The DCRS2 polypeptide is also useful for modulating cell
CC proliferation, for diagnostic and therapeutic applications, for
CC detecting presence of their ligands and in drug screening assays. It
CC is also useful for treating conditions such as immunological disorders.
CC The present sequence represents a cytokine receptor subunit protein
CC which is given in an alignment of various cytokine receptor subunits in
CC the exemplification of the present invention.
XX
SQ Sequence 422 AA;

Query Match 100.0%; Score 2275; DB 22; Length 422;
Best Local Similarity 100.0%; Pred. No. 1.2e-150;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSSSCSLSRVLVAVATALVSASSPCQAWPGVQYGPGRSVKLCPCGVTAGDPVSWF 60
Db 1 MSSSCSLSRVLVAVATALVSASSPCQAWPGVQYGPGRSVKLCPCGVTAGDPVSWF 60

QY 61 RGEPEKLLQGPDSGLGHELVLQAADSTDEGTYICQTLDGALGCTVTLQLGYPARPVWSC 120
Db 61 RGEPEKLLQGPDSGLGHELVLQAADSTDEGTYICQTLDGALGCTVTLQLGYPARPVWSC 120

QY 121 QAADYENFSCWTSPSOISGLPTRYLTYSRKKTVLGADSORRSPSTGWPCCQDPLGAARC 180
Db 121 QAADYENFSCWTSPSOISGLPTRYLTYSRKKTVLGADSORRSPSTGWPCCQDPLGAARC 180

QY 181 VHGAEFWQYRINVTENVPLGASTRLLDVLSQISILRPDPQGLRVESVPGYPRRLRASW 240
Db 181 VHGAEFWQYRINVTENVPLGASTRLLDVLSQISILRPDPQGLRVESVPGYPRRLRASW 240

QY 241 TYPASWPCOPHFLLKFRLOYRPAQHPAWSTVEPAGLEEVIDAVAGLPHAVRVASRDFLD 300
Db 241 TYPASWPCOPHFLLKFRLOYRPAQHPAWSTVEPAGLEEVIDAVAGLPHAVRVASRDFLD 300

QY 301 AGTWSTWSPAEANGTPTGTIPKEIPAWGOLHTQPEVEPOVDSPPAPRPSLQHPRLLDHR 360
Db 301 AGTWSTWSPAEANGTPTGTIPKEIPAWGOLHTQPEVEPOVDSPPAPRPSLQHPRLLDHR 360

RESULT 5
AAR92814
ID AAR92814 standard; Protein; 423 AA.
XX
AAR92814;
XX
DT 21-MAY-1996 (first entry)

```

XX DE Human interleukin-11 receptor alpha chain.
XX DE
XX KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
XX KW therapy; diagnosis.
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..23
XX FT Protein /label= Sig_peptide
XX FT Domain /label= Mat_protein
XX FT /label= Extracellular_domain
XX FT /note= "the extracellular domain includes
XX FT haemopoietin and Ig-like domains"
XX FT
XX FT Domain 367..392
XX FT /label= Transmembrane_domain
XX FT Domain 393..423
XX FT /label= Cytoplasmic_tail
XX
XX PN WO9607737-A1.
XX
XX PD 14-MAR-1996.
XX
XX PF 05-SEP-1995; 95WO-AU00578.
XX
XX PR 05-SEP-1994; 94AU-0007902.
XX PR 05-SEP-1994; 94AU-0007901.
XX
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX PI Hilton DJ;
XX
XX DR WPI; 1996-171612/17.
XX DR N-PSDB; AAT17869.
XX
XX PT Nucleic acid encoding haemopoietin receptor containing conserved
XX PT amino acid motif esp. IL-11 receptor alpha chain - used for
XX PT developing IL-11 (ant)agonists
XX
XX PS Claim 8; Page 47-49; 87pp; English.
XX
XX CC The human interleukin-11 (IL-11) receptor alpha chain (AAR92814)
XX CC was identified by expression of DNA (AAT17869) isolated from human
XX CC bone marrow cDNA libraries. Expression of the human IL-11
XX CC receptor alpha chain results in specific-binding of human IL-11
XX CC and permits IL-11 signalling. The receptor alpha chain can be used
XX CC to develop agonists or antagonists of therapeutic appln. or in
XX CC the treatment or diagnosis of conditions involving a deficiency of
XX CC IL-11, excess IL-11 or aberrant effects of normal endogenous IL-11
XX CC levels.
XX
XX SQ Sequence 423 AA;
XX
XX Query Match 99.2%; Score 2257.5; DB 17; Length 423;
XX Best Local Similarity 99.5%; Pred. No. 1.9e-149;
XX Matches 421; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
XX
XX QY 1 MSSSCGSLRVLVAVATALVSASSPCQAWGPPGVQYQGPGRSVKLCPCGVTAGDPVSWF 60
XX Db |
XX 1 MSSSCGSLRVLVAVATALVSASSPCQAWGPPGVQYQGPGRSVKLCCEGVTAGDPVSWF 60
XX
XX QY 61 RDGEPKLLQGPDSGLGHELVLAQAQSTDEGTVCITQDLGALGGTVTQLQGYPPARPVVSC 120
XX Db |
XX 61 RDGEPKLLQGPDSGLGHELVLAQAQSTDEGTVCITQDLGALGGTVTQLQGYPPARPVVSC 120
XX
XX QY 121 QAADYENFSCWSPSQISGLPRYLTYSRKKTVLGADSORRSPSTGPPCPQDPLGAARC 180
XX Db |
XX 121 QAADYENFSCWSPSQISGLPRYLTYSRKKTVLGADSORRSPSTGPPCPQDPLGAARC 180
XX
XX QY 181 VVHGAEFWSQYRINTEVNPL-GASTRLLDVSLQSLTRDPDPPQGLRVESVPCYPRGLRAS 239

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Db 181 VVHGAEFWSQYRINTEVNPLGGASTRLLDVSLQSLTRDPDPPQGLRVESVPCYPRGLRAS 240
QY 240 WTYPASWPCQPHFLKFRLOYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFL 299
Db 241 WTYPASWPCQPHFLKFRLOYRPAQHPAWSTVEPAGLEEVITDAVAGLPHAVRVASARDFL 300
QY 300 DAGTWTSTWSPAWGTPSTGTIPKEIPAWGQLHTQPEVEPQVDSPAPPRPSLOPHPRLLDH 359
Db 301 DAGTWTSTWSPAWGTPSTGTIPKEIPAWGQLHTQPEVEPQVDSPAPPRPSLOPHPRLLDH 360
QY 360 RDSVEQVAVLASLGLSFLGLVAGALALGLWLRLRRGKGDKSPKGFASVIPVDRRPGA 419
Db 361 RDSVEQVAVLASLGLSFLGLVAGALALGLWLRLRRGKGDKSPKGFASVIPVDRRPGA 420
QY 420 PNL 422
Db 421 PNL 423
Db 421 PNL 423

RESULT 6
AAR92813
ID AAR92813. standard; Protein; 432 AA.
XX
XX AAR92813;
XX
XX DT 21-MAY-1996 (first entry)
XX
XX DE Murine interleukin-11 receptor alpha chain.
XX
XX KW Haemopoietin; interleukin-11; IL-11; receptor; agonist; antagonist;
XX KW therapy; diagnosis.
XX
XX OS Mus sp.
XX
XX FH Key Location/Qualifiers
XX FT Peptide 1..23
XX FT Protein /label= Sig_peptide
XX FT /label= Mat_protein
XX FT Domain 24..367
XX FT /label= Extracellular_domain
XX FT /note= "the extracellular domain includes
XX FT haemopoietin and Ig-like domains"
XX FT
XX FT Domain 368..393
XX FT /label= Transmembrane_domain
XX FT Domain 394..432
XX FT /label= Cytoplasmic_tail
XX
XX PN WO9607737-A1.
XX PD 14-MAR-1996.
XX
XX PF 05-SEP-1995; 95WO-AU00578.
XX
XX PR 05-SEP-1994; 94AU-0007902.
XX PR 05-SEP-1994; 94AU-0007901.
XX
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX PI Hilton DJ;
XX
XX DR WPI; 1996-171612/17.
XX DR N-PSDB; AAT17868.
XX
XX PT Nucleic acid encoding haemopoietin receptor containing conserved
XX PT amino acid motif esp. IL-11 receptor alpha chain - used for
XX PT developing IL-11 (ant)agonists
XX
XX PS Claim 6; Page 42-44; 87pp; English.
XX
XX CC The murine interleukin-11 (IL-11) receptor alpha chain Nr1
XX CC (AAR92813) was identified by expression of DNA (AAT17868) isolated

```

CC from adult mouse liver cDNA libraries. Nrl is a low affinity
 CC receptor for IL-11 and interacts with gpl30 to generate a high
 CC affinity IL-11 receptor. Il-11 can be used to develop
 CC agonists or antagonists of therapeutic appln. or in the treatment
 CC or diagnosis of conditions involving a deficiency of IL-11,
 CC excess IL-11 or aberrant effects of normal endogenous IL-11
 CC levels.
 XX
 SQ Sequence 432 AA;

Query Match 83.4%; Score 1897; DB 17; Length 432;
 Best Local Similarity 83.5%; Pred. No. 2.7e-124;
 Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1;

QY 1 MSSCSGLRLVAVATLVASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSWF 60
 DB 1 MSSCSGLTRVLVAVATLVSSSPCQAWGPPGVQYQGRVPMVLCPCGVSAGTPVSWF 60

QY 61 RDGEFKLQGPDSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQLGYPARPVYSC 120
 DB 61 RDGSRLLQGPDSGLGHELVLAQVDSDEGTYVCOITLDVSGGMVTLKLGPPARPVYSC 120

QY 121 QAADYENFSCWSPQISGLPTRYLTYSYRKTVLGADSORRSPSTGPPWPCQDPPLGAARC 180
 DB 121 QAADYENFSCWSPQISGLPTRYLTYSYRKTLPCAESQRESPTGPPWPCQDPPLGAARC 180

QY 181 VVHGAEFWSQRYINTEVNPGLGASTRLDVSILQSLRPDPQGLRVESVPGYPRRLRASW 240
 DB 181 VVHGAEFWSQRYINTEVNPGLGASTRLDVSILQSLRPDPQGLRVESVPGYPRRLHASW 240

QY 241 TYPASWPCQPHFLKFRQYRPAQHPAWSTVEPIGLEEVITDVAAGLPHAVRVSARDFLD 300
 DB 241 TYPASWPCQPHFLKFRQYRPAQHPAWSTVEPIGLEEVITDVAAGLPHAVRVSARDFLD 300

QY 301 AGTWSTWSPAWGTPSTGTIPKEIPAWGQLHTQ--PEVEPQVDSPPAPRPSLQPHRLLD 358
 DB 301 AGTWSAWEAAGTPSTGTIPKEIPAWGQLHTQ--PEVEPQVDSPPAPRPSLQPHRLLD 360

QY 359 HRDSVEQAVLASGLISFLGLVAGALALGLWLRRLRGKDGSPKPGFLASVIVDRRPG 418
 DB 361 HRDPLEQAVLASGLISFLGLVAGALALGLWLRRLRGKDGSPKPGFLASVIVDRRPG 420

QY 419 APNL 422
 DB 421 IPNL 424

RESULT 7
 AAB36653
 ID AAB36653 standard; Protein; 432 AA.
 AC AAB36653;
 XX
 XX 13-MAR-2001 (first entry)
 DE Mouse IL-11 receptor subunit alpha protein SEQ ID NO:10.
 XX
 KW DNAX cytokine receptor subunit; DCRS2; receptor protein;
 KW modulating cell proliferation; diagnosis; detection; drug screening;
 KW immunological disorder.
 OS Mus sp.
 XX
 XX WQ200073451-A1.
 PN 07-DEC-2000.
 PD
 XX
 XX 30-MAY-2000; 2000WO-US14867.
 PF
 XX
 XX 01-JUN-1999; 99US-0322913.
 PR
 XX
 XX (SCHE) SCHERING CORP.
 PA
 XX
 XX

PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
 XX WPI; 2001-061536/07.
 DR
 XX
 XX Novel composition comprising DNAX cytokine receptor subunit polypeptide
 PT useful for regulating immune system function and for treating
 PT immunological disorders -
 XX
 XX Disclosure; Page 13-15; 93pp; English.

XX The present invention describes a composition (I) comprising a
 CC recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide.
 CC The DCRS2 polypeptide is useful for binding ligands and for preparing
 CC antibodies. The DCRS2 polypeptide is also useful for modulating cell
 CC proliferation, for diagnostic and therapeutic applications, for
 CC detecting presence of their ligands and in drug screening assays. It
 CC is also useful for treating conditions such as immunological disorders.
 CC The present sequence represents a cytokine receptor subunit protein
 CC which is given in an alignment of various cytokine receptor subunits in
 CC the exemplification of the present invention.

XX SQ Sequence 432 AA;

Query Match 82.2%; Score 1871; DB 22; Length 432;
 Best Local Similarity 82.5%; Pred. No. 1.8e-122;
 Matches 350; Conservative 19; Mismatches 53; Indels 2; Gaps 1;

QY 1 MSSCSGLRLVAVATLVASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSWF 60
 DB 1 MSSCSGLTRVLVAVATLVSSSPCQAWGPPGVQYQGRVPMVLCPCGVSAGTPVSWF 60

QY 61 RDGEFKLQGPDSGLGHELVLAQADSTDEGTYICOTLDGALGGTTLQLGYPARPVYSC 120
 DB 61 RDGSRLLQGPDSGLGHELVLAQVDSDEGTYVCOITLDVSGGMVTLKLGPPARPVYSC 120

QY 121 QAADYENFSCWSPQISGLPTRYLTYSYRKTVLGADSORRSPSTGPPWPCQDPPLGAARC 180
 DB 121 QAADYENFSCWSPQISGLPTRYLTYSYRKTLPCAESQRESPTGPPWPCQDPPLGAARC 180

QY 181 VVHGAEFWSQRYINTEVNPGLGASTRLDVSILQSLRPDPQGLRVESVPGYPRRLRASW 240
 DB 181 VVHGAEFWSQRYINTEVNPGLGASTRLDVSILQSLRPDPQGLRVESVPGYPRRLHASW 240

QY 241 TYPASWPCQPHFLKFRQYRPAQHPAWSTVEPIGLEEVITDVAAGLPHAVRVSARDFLD 300
 DB 241 TYPASWPCQPHFLKFRQYRPAQHPAWSTVEPIGLEEVITDVAAGLPHAVRVSARDFLD 300

QY 301 AGTWSTWSPAWGTPSTGTIPKEIPAWGQLHTQ--PEVEPQVDSPPAPRPSLQPHRLLD 358
 DB 301 AGTWSAWEAAGTPSTGTIPKEIPAWGQLHTQ--PEVEPQVDSPPAPRPSLQPHRLLD 360

QY 359 HRDSVEQAVLASGLISFLGLVAGALALGLWLRRLRGKDGSPKPGFLASVIVDRRPG 418
 DB 361 HRDPLEQAVLASGLISFLGLVAGALALGLWLRRLRGKDGSPKPGFLASVIVDRRPG 420

QY 419 APNL 422
 DB 421 IPNL 424

RESULT 8
 AAR99091
 ID AAR99091 standard; Protein; 441 AA.
 XX
 AC AAR99091;
 XX
 XX 09-OCT-1996 (first entry)
 DT Murine Etl-2 gene product.
 DE
 DE Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;
 KW osteoporosis; Paget disease; myeloma; Etl-2.
 KW
 XX

Db 265 FRLOYPQAHPAWSTVEPIGLEEVITDAVAGLPHAVRVVSARDFLDAGTWSAWEAWGTP 324
 QY 316 STGTIPKEIPAWGQLHTQ--PEVEPQVDSPPAPRPSLQHPRLLDHRDSVEQVAVLASLG 373
 Db 325 STGTIPKEIPAWGQLHTQ--PEVEPQVDSPPAPRPSLQHPRLLDHRDSVEQVAVLASLG 384
 QY 374 ILSFGLVAGALALGLWLRGGKDGSPKPGFLASVIPVDRPGAPNL 422
 Db 385 IFSCGLGAVGALALGLWLRGGKDGSPKPGFLASVIPVDRPGAPNL 433

RESULT 10
 AAEL14614
 ID AAEL14614 standard; Protein; 441 AA.
 AC AAEL14614;
 XX
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Murine Etl-2 protein.
 KW Murine; Etl-2; interleukin-11 receptor; IL-11R; immune deficiency;
 KW haematopoietic progenitor cell; cancer; bone loss; osteoporosis;
 KW Paget's disease; multiple myeloma; hypogonadal condition.
 OS Mus sp.
 XX
 XX US6350855-B1.
 PD 26-FEB-2002.
 XX
 PF 15-SEP-1997; 97US-0929846.
 XX
 PR 14-JUN-1996; 96US-0663584.
 PR 22-DEC-1994; 94US-0362304.
 XX
 PA (GEMY) GENETICS INST INC.
 XX
 PI Tobin J;
 XX
 DR WPI; 2002-215268/27.
 DR N-PSDB; AAD27929.
 XX
 PT Novel isolated human interleukin-11 receptor protein useful in assays
 PT to screen for binding agents and for treating immune deficiencies,
 PT cancer and bone related disorders, e.g., osteoporosis
 XX
 PS Disclosure; Column 25-28; 20pp; English.
 XX
 CC The invention relates to human interleukin-11 receptor (IL-11R). The
 CC IL-11R is involved in the regulation of immune system by interaction
 CC with IL-11. The IL-11R polypeptide may be used to screen for agents that
 CC bind to it or interfere with the binding of IL-11, as diagnostic agent
 CC for detecting the expression or presence of IL-11R, IL-11 or cells
 CC expressing IL-11R or IL-11. The IL-11R and IL-11R inhibitors may be
 CC useful in treatment or modulation of IL-11-related conditions which
 CC include immune deficiencies, specifically deficiencies in haematopoietic
 CC progenitor cells, or related disorders, cancer and other diseases.
 CC It is also believed that IL-11 and IL-11R may play a role in the
 CC regulation of bone maturation and repair. As a result, human IL-11R
 CC protein and IL-11R inhibitors may be useful in treatment of bone loss
 CC (including that associated with osteoporosis, post-menopausal
 CC osteoporosis, senile osteoporosis, idiopathic osteoporosis, Paget's
 CC disease, multiple myeloma and hypogonadal conditions). The present
 CC sequence is murine Etl-2, used to illustrate the invention.
 XX
 SQ Sequence 441 AA;

Query Match 80.5%; Score 1831; DB 23; Length 441;
 Best Local Similarity 83.1%; Pred. No. 1.le-119;
 Matches 340; Conservative 17; Mismatches 50; Indels 2; Gaps 1;
 QY 16 ATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSVFRDGPRLQGPDSGL 75

Db 25 ATALVSASSPCQAWGPPGVQYQGRSVKLCPCGVTAGDPVSVFRDGPRLQGPDSGL 84
 QY 76 GHLEVLQAQADSTDEGTYYICQTLDDGALGGVNTQLQGYPPARPVVSQAAADYENFSCWTSPS 135
 Db 85 GHRLVLAQVDSDEGTYYVCQTLDDGSGGMVTLKLGFPARPPEVSQAVDYENFSCWTSPG 144
 QY 136 QISGLPTRYLTYSRKKTVLGADSORRSPSTGPPWCPQDPLGAARCVVHGAETWSOYRINV 195
 Db 145 QVSGLPTRYLTYSRKKTLPGAESQRESPTGPPWCPQDPLEASRCVVHGAETWSEYRINV 204
 QY 196 TEVNPGLASTRLLDVLSQILRPDPQGLRVESVPGYPRRLRASWTYPASWPCQPHFLK 255
 Db 205 TEVNPGLASTRLLDVLSQILRPDPQGLRVESVPGYPRRLHASWTYPASWRRQPHFLK 264
 QY 256 FRLOYPQAHPAWSTVEPIGLEEVITDAVAGLPHAVRVVSARDFLDAGTWSAWEAWGTP 315
 Db 265 FRLOYPQAHPAWSTVEPIGLEEVITDAVAGLPHAVRVVSARDFLDAGTWSAWEAWGTP 324
 QY 316 STGTIPKEIPAWGQLHTQ--PEVEPQVDSPPAPRPSLQHPRLLDHRDSVEQVAVLASLG 373
 Db 325 STGTIPKEIPAWGQLHTQ--PEVEPQVDSPPAPRPSLQHPRLLDHRDSVEQVAVLASLG 384
 QY 374 ILSFGLVAGALALGLWLRGGKDGSPKPGFLASVIPVDRPGAPNL 422
 Db 385 IFSCGLGAVGALALGLWLRGGKDGSPKPGFLASVIPVDRPGAPNL 433

RESULT 11
 AAY59390
 ID AAY59390 standard; Protein; 379 AA.
 XX
 AC AAY59390;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Murine soluble interleukin-11 receptor.
 XX
 KW Interleukin-11; IL-11; IL-11R; human; bone density disorder; gp130;
 KW IL-11 tertiary complex; glycoprotein 130; postmenopausal bone loss;
 KW bone resorption inhibitor; bone formation; therapy.
 XX
 OS Mus sp.
 XX
 PN WO9959608-A2.
 XX
 PD 25-NOV-1999.
 XX
 PF 19-MAY-1999; 99WO-CA00516.
 XX
 PR 19-MAY-1998; 98CA-2237915.
 XX
 PA (HAMI-) HAMILTON CIVIC HOSPITAL RES DEV CORP.
 XX
 PI Shaughnessy S, Austin RC;
 XX
 DR WPI; 2000-062377/05.
 DR N-PSDB; AAZ40400.
 XX
 XX Inhibiting formation of a tertiary complex for the treatment of
 PT osteoporosis
 XX
 PS Example 3; Page 46-50; 61pp; English.
 XX
 CC This sequence is the soluble mouse interleukin-11 receptor (IL-11R).
 CC The invention relates to a method of treating or alleviating the symptoms
 CC of a pathological condition in which bone density is decreased comprises
 CC inhibiting the formation of a tertiary complex of IL-11, IL-11 receptor
 CC and glycoprotein 130 (gp130) in a mammalian patient suffering from such a
 CC condition. The method is used to treat or alleviate the symptoms of a
 CC pathological condition in which bone density is decreased, especially
 CC postmenopausal bone loss. The IL-11 binding peptide is useful in the
 CC purification of IL-11 or in depleting IL-11 from a solution. TRAP


```
XX Soluble; sIL-6R.
XX Mus musculus.
XX Key Location/Qualifiers
XX Peptide 1..19
XX Region /label= sig_peptide
XX 358..385
XX /note= "see CC"
XX
XX JP04099800-A.
XX 31-MAR-1992.
XX
XX 17-AUG-1990; 90JP-0215886.
XX
XX 17-AUG-1990; 90JP-0215886.
XX (CHUS ) CHUGAI PHARM CO LTD.
XX (TOYJ ) TOSOH CORP.
XX
XX WPI; 1992-157367/19.
XX P-PSDB; AAR22616.
XX
XX Recombinant mouse IL-6 receptor - prepd. by culturing host
XX transformed by expression vector contg. DNA coding the protein,
XX and collecting soluble prod.
XX
XX Disclosure; Fig 7(1-2); 9pp; Japanese.
XX
XX The sequence is the full-length mouse IL-6 receptor.
XX The region comprising amino acids 358-385 (see feature table)
XX is indicated but not labelled in the sequence given in the
XX specification. The sequence is used in the prodn. of a sol.
XX mouse IL-6 receptor protein (sIL-6R) which binds specifically to
XX IL-6 and has no intracellular region.
XX
XX Sequence 460 AA;
XX
XX Query Match 17.4%; Score 395.5; DB 13; Length 460;
XX Best Local Similarity 30.7%; Pred. No. 1.4e-19;
XX Matches 145; Conservative 58; Mismatches 178; Indels 91; Gaps 25;
XX
XX 1 MSSSCSLRVLVAVATALYSASSPCQANGPPGVQGVQGRSVKLCPCGVTAGDPVSV-- 58
XX 2 LTVGCTLLVALLAAPAVLVLS--CRALEVANGTVTSLEGATVTLICPGKEAGNVTHI 59
XX
XX 59 WFRDGEFKLQGPD-SGLGHVLAQADSTDEGTYICQTLDGALGGTVTLQLGYPARPV 117
XX 60 WYISGS----QNRWTTTGNVLVRDVLQSDTGDYLC-SLNDHLVGVTVPLLDVPPPEPK 114
XX
XX 118 VSC-QAADYENFSCWSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGFWPCP-QDPL 175
XX 115 LSCFRKNPLNAICEWRPSTPS-PTTKAVLFAKKI-----NTNGKSDFOVPCQYSQQL 168
XX
XX 176 GAARCVVHGAEFWSQYRI-NVTEVNPGLASTRLDV--SLQSTILRDPDPOGLRVESVPGY 232
XX 169 KSFCQVEILGDKVHIIVSLCVANSVGSKSHNEAFSLK-MVQDPPANLVVSAIPGR 227
XX
XX 233 PRLRASWTYPASWPCOPHFLKRLQYRPAQHPAMS-----TVEPAGLEEIVITDAVAG 286
XX 228 PRWLKVSQHPETWD-PSYLLQFQLRYR----PVMSKEFTVLLLPVAQYQCVIDHALRG 282
XX
XX 287 LPHAVRVSARDFLDAGTWSTWSEAMGTPTGTIPKEIPA---WGQLHTQPEVPEQVDS 343
XX 283 VKHVQVVRGKEELDGLGOWSEWSEPTGTPIAE-PRTPAGILWNP--TQVSVE---DS- 335
XX
XX 344 APPRPSLQPHRLDHRD-----SVEQVAVLA-----SGLSFLGLVACALALGLM--- 390
XX 336 -----ANHEDQYESTEATSVLAPVQESSMSLPTFL-VAGSLAFGLLLCV 381
XX
XX 391 ---LRLRRGKD-----GSPKPGFLASVIPVDRRPGAPN 421
XX
XX Db 382 FIILRLQKWKSEAKESKTTSPPPPPYSLGPLKPTTELLVPLTPHSSGSDN 433
XX
XX RESULT 14
XX AAB36656
XX ID AAB36656 standard; Protein; 460 AA.
XX AC AAB36656;
XX
XX DT 13-MAR-2001 (first entry)
XX
XX Mouse IL-6 receptor subunit alpha protein SEQ ID NO:13.
XX
XX DNAX cytokine receptor subunit; DCRS2; receptor protein;
XX modulating cell proliferation; diagnosis; detection; drug screening;
XX immunological disorder.
XX
XX Mus sp.
XX
XX WO200073451-A1.
XX
XX 07-DEC-2000.
XX
XX 30-MAY-2000; 2000WO-US14867.
XX
XX 01-JUN-1999; 99US-0322913.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FJ;
XX WPI; 2001-061536/07.
XX
XX Novel composition comprising DNAX cytokine receptor subunit polypeptide
XX useful for regulating immune system function and for treating
XX immunological disorders
XX
XX Disclosure; Page 13-15; 93pp; English.
XX
XX The present invention describes a composition (I) comprising a
XX recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide.
XX The DCRS2 polypeptide is useful for binding ligands and for preparing
XX antibodies. The DCRS2 polypeptide is also useful for modulating cell
XX proliferation, for diagnostic and therapeutic applications, for
XX detecting presence of their ligands and in drug screening assays. It
XX is also useful for treating conditions such as immunological disorders.
XX The present sequence represents a cytokine receptor subunit protein
XX which is given in an alignment of various cytokine receptor subunits in
XX the exemplification of the present invention.
XX
XX Sequence 460 AA;
XX
XX Query Match 17.4%; Score 395.5; DB 22; Length 460;
XX Best Local Similarity 30.7%; Pred. No. 1.4e-19;
XX Matches 145; Conservative 58; Mismatches 178; Indels 91; Gaps 25;
XX
XX 1 MSSSCSLRVLVAVATALYSASSPCQANGPPGVQGVQGRSVKLCPCGVTAGDPVSV-- 58
XX 2 LTVGCTLLVALLAAPAVLVLS--CRALEVANGTVTSLEGATVTLICPGKEAGNVTHI 59
XX
XX 59 WFRDGEFKLQGPD-SGLGHVLAQADSTDEGTYICQTLDGALGGTVTLQLGYPARPV 117
XX 60 WYISGS----QNRWTTTGNVLVRDVLQSDTGDYLC-SLNDHLVGVTVPLLDVPPPEPK 114
XX
XX 118 VSC-QAADYENFSCWSPSQISGLPTRYLTSYRKKTVLGADSORRSPSTGFWPCP-QDPL 175
XX 115 LSCFRKNPLNAICEWRPSTPS-PTTKAVLFAKKI-----NTNGKSDFOVPCQYSQQL 168
XX
XX 176 GAARCVVHGAEFWSQYRI-NVTEVNPGLASTRLDV--SLQSTILRDPDPOGLRVESVPGY 232
XX 169 KSFCQVEILGDKVHIIVSLCVANSVGSKSHNEAFSLK-MVQDPPANLVVSAIPGR 227
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